

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 19, 2004, 15:47:57 ; Search time 11.5 Seconds  
(without alignments)  
66.916 Million cell updates/sec

Title: VARIANT2  
Perfect score: 25  
Sequence: 1 XQXXVXHI 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 148

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78: \*  
2: p1r1: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	52.0	8	2 A31570	angiotensin-conver
2	13	52.0	8	2 A61496	ubiquitin - celer
3	13	52.0	8	2 S53008	citrate synthase -
4	12	48.0	8	2 PT0368	Ig gamma chain C r
5	12	48.0	8	2 A42689	major postsynaptic
6	10	40.0	8	2 T14906	hypothetical prote
7	10	40.0	8	2 PH1618	Ig H chain V-D-J r
8	10	40.0	8	2 B47594	aspartate kinase (
9	9	36.0	8	2 XGHUEU	urine glycopeptide
10	9	36.0	8	2 S43971	tumor-associated a
11	9	36.0	8	2 S43972	tumor-associated a
12	9	36.0	8	2 T10077	hypothetical prote
13	9	36.0	8	2 S68802	nitrate reductase
14	9	36.0	8	2 PQ0726	unidentified 4.5/4
15	9	36.0	8	2 JS0316	leucokinin VI - Ma
16	9	36.0	8	2 B45800	serum albumin - do
17	9	36.0	8	2 A54823	olfactory receptor
18	9	36.0	8	2 B54823	olfactory receptor
19	9	36.0	8	2 S65381	cytochrome-c oxida
20	9	36.0	8	2 S69165	ferredoxin a2 - Ja
21	9	36.0	8	2 A25836	L-serine ammonia-1
22	9	32.0	8	2 B24749	neuropeptide B - b
23	8	32.0	8	2 S19288	acylase - Kluyvera
24	8	32.0	8	2 S70727	ibpf protein - Shi
25	8	32.0	8	2 S63493	disintegrin - bull
26	8	32.0	8	2 PA0035	protein QA300039 -
27	8	32.0	8	2 T10952	hypothetical prote
28	8	32.0	8	2 S78036	ribosomal protein
29	8	32.0	8	2 PT0030	inulinase (EC 3.2.

30	8	32.0	8	2 PL0162	paramyosin - north
31	8	32.0	8	2 A46306	spasmodic toxin
32	8	32.0	8	2 A14683	aspartate transami
33	8	32.0	8	2 PT0298	Ig heavy chain CRD
34	8	32.0	8	2 PT0323	Ig heavy chain CRD
35	8	32.0	8	2 PM0043	phosphatidylethano
36	8	32.0	8	2 A49404	prealbumin - weste
37	8	32.0	8	2 C39690	neural cell adhesi
38	8	32.0	8	2 A35180	neutral protease
39	8	32.0	8	2 PC4372	telomeric and tetr
40	8	32.0	8	2 S29272	tocopherol-binding
41	7	28.0	8	2 A61348	red pigment-concen
42	7	28.0	8	2 A28004	adipokinetic hormo
43	7	28.0	8	2 S08995	hypertrehalosemic
44	7	28.0	8	2 S08996	hypertrehalosemic
45	7	28.0	8	2 S10596	adipokinetic hormo

#### ALIGNMENTS

RESULT 1  
A31570  
angiotensin-converting enzyme inhibitor - yellowfin tuna  
C/Species: Thunnus albacares (yellowfin tuna)  
C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 18-Aug-2000  
C/Accession: A31570  
R/Konuma, Y.; Matsunoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.  
Biochem. Biophys. Res. Commun. 155, 332-337, 1988  
A/Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.  
A/Accession number: A31570; PMID:88326322; PMID:3415688  
A/Accession: A31570  
A/Molecule type: protein  
A/Residues: 1-8 <KOH>  
A/Note: the source is designated as Neothunnus macropterus  
C/Keywords: angiotensin-converting enzyme inhibitor

Query Match 52.0%; Score 13; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHI 8  
DB 2 TH1 4

#### RESULT 2

A61496  
ubiquitin - celer (fragment)  
C/Species: Apium graveolens (celer)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 07-May-1999  
C/Accession: A61496  
R/Goldstein, G.; Scheid, M.; Hammerling, U.; Boyse, E.A.; Schlessinger, D.H.; Niall, H.D.  
Proc. Natl. Acad. Sci. U.S.A. 72, 11-15, 1975  
A/Title: Isolation of a polypeptide that has lymphocyte-differentiating properties and is  
A/Reference number: A61496; PMID:75120426; PMID:1078892  
A/Accession: A61496  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-8 <GOL>  
A/Note: a small amount of material was sequenced; the amino-terminal residue is unlikely

Query Match 52.0%; Score 13; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXV 6  
DB 1 XQIXV 6

#### RESULT 3

SS3008  
 citrate synthase - cucurbit  
 C/Species: Cucurbita sp. (cucurbit)  
 C/Date: 14-Jul-1995 #sequence\_revision 03-Nov-1995 #text\_change 17-Mar-1999  
 C/Accession: SS3008  
 R/Rato, A.; Hayashi, M.; Mori, H.; Nishimura, M.  
 Plant Mol. Biol. 27, 377-390, 1995  
 A/Title: Molecular characterization of a glyoxysomal citrate synthase that is synthesized  
 A/Reference number: SS3007; PMID:95195164; PMID:7888626  
 A/Accession: SS3008  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-8 <KAT>

Query Match 52.0%; Score 13; DB 2; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6  
 :|:|:  
 Db 2 AQTWVA 7

RESULT 4  
 PT0368  
 Ig gamma chain C region (gamma-1) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Aug-1996  
 C/Accession: PT0368  
 R/Milli, M.; Fougereau, M.; Guglielmi, P.; Schiffr, C.  
 Mol. Immunol. 28, 753-761, 1991  
 A/Title: Early occurrence of immunoglobulin isotype switching in human fetal liver.  
 A/Reference number: PT0368; PMID:91312348; PMID:1906981  
 A/Accession: PT0368  
 A/Molecule type: mRNA  
 A/Residues: 1-8 <MTL>  
 A/Experimental source: fetal liver  
 C/Keywords: immunoglobulin

Query Match 48.0%; Score 12; DB 2; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6  
 :|:|:  
 Db 2 HOGPIG 7

RESULT 5  
 A42689  
 major postsynaptic density protein - rat (fragment)  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 26-May-1994  
 C/Accession: A42689  
 R/Mu, K.; Huang, Y.; Adler, J.; Black, I.B.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 3015-3019, 1992  
 A/Title: On the identity of the major postsynaptic density protein.  
 A/Reference number: A42689; PMID:92212958; PMID:1113576  
 A/Accession: A42689  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-8 <WDA>

Query Match 48.0%; Score 12; DB 2; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHI 8  
 :|:|:  
 Db 2 LKVPNI 7

RESULT 6

T14906  
 hypothetical protein - parsley  
 C/Species: Petroselinum crispum (parsley)  
 C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C/Accession: T14906  
 R/Feldbrugge, M.; Sprenger, M.; Dinkelbach, M.; Yazaki, K.; Hatter, K.; Weishaar, B.  
 Plant Cell 6, 1607-1621, 1994  
 A/Title: Functional analysis of a light-responsive plant bZIP transcriptional regulator.  
 A/Reference number: T14906; PMID:95128172; PMID:7827494  
 A/Accession: T14906  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-8 <FBL>  
 A/Cross-references: EMBL:575395; NID:9913201; PID:e194245

Query Match 40.0%; Score 10; DB 2; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VXXH 7  
 :|:  
 Db 1 MKH 3

RESULT 7  
 PH1618  
 Ig H chain V-D-J region (clone B-1ess 33) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C/Accession: PH1618  
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A/Reference number: PH1580; PMID:93301609; PMID:8315387  
 A/Accession: PH1618  
 A/Molecule type: DNA  
 A/Residues: 1-8 <LEV>  
 A/Experimental source: bone marrow pre-B lymphocyte  
 C/Keywords: immunoglobulin

Query Match 40.0%; Score 10; DB 2; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 XVXH 7  
 :|:  
 Db 1 CARH 4

RESULT 8  
 B47594  
 aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain N13) (fragment)  
 C/Species: Corynebacterium flavum  
 C/Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 19-Dec-1997  
 C/Accession: B47594  
 R/Follettie, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinskey, A.J.  
 J. Bacteriol. 175, 4096-4103, 1993  
 A/Title: Gene structure and expression of the Corynebacterium flavum N13 ask-ase operon.  
 A/Reference number: A47594; PMID:93308089; PMID:8100567  
 A/Accession: B47594  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: DNA  
 A/Residues: 1-8 <FOL>  
 C/Keywords: phosphotransferase

Query Match 40.0%; Score 10; DB 2; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6  
 :|:|:  
 Db 1 MERAIVL 6

## RESULT 9

XGHEU  
 urine glycopeptide - human  
 C/Species: Homo sapiens (man)  
 C/Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
 C/Accession: A03188  
 R/Lote, C.J.; Weiss, J.B.  
 Blochem. J. 123:25P, 1971  
 A/Title: Identification in urine of a low-molecular-weight polar glycopeptide containing  
 A/Reference number: A03188; PMID:72062338; PMID:5126885  
 A/Accession: A03188  
 A/Molecule type: protein  
 A/Residues: 1-8 <LOT>  
 C/Comment: The identity of the glycoprotein from which this peptide is derived is unknown  
 re has also been found (see PIR:XGHEU).  
 C/Superfamily: unassigned animal peptides  
 C/Keywords: glycoprotein  
 F/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7  
 : : :  
 Db 2 EH 3

## RESULT 10

S43971  
 tumor-associated antigen MUT1 - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 20-Oct-1994 #sequence\_revision 17-Nov-1995 #text\_change 18-Aug-2000  
 C/Accession: S43971  
 R/Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.  
 Nature 369, 67-71, 1994  
 A/Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine  
 A/Reference number: S43971; PMID:94217811; PMID:8164742  
 A/Accession: S43971  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-8 <MAN>  
 C/Superfamily: unassigned animal peptides

Query Match 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;

Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXV 6  
 : : :  
 Db 2 EQNTAQ 7

## RESULT 11

S43972  
 tumor-associated antigen MUT2 - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 20-Oct-1994 #sequence\_revision 17-Nov-1995 #text\_change 18-Aug-2000  
 C/Accession: S43972  
 R/Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.  
 Nature 369, 67-71, 1994  
 A/Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine  
 A/Reference number: S43971; PMID:94217811; PMID:8164742  
 A/Accession: S43972  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-8 <MAN>  
 C/Superfamily: unassigned animal peptides

Query Match 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXV 6  
 : : :  
 Db 2 EQNTAQ 7

## RESULT 12

T10077  
 hypothetical protein N - Methylophilus methylotrophus (fragment)  
 C/Species: Methylophilus methylotrophus  
 C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
 C/Accession: T10077  
 R/Chistoserdov, A.V.; McIntire, W.S.; Mathews, F.S.; Lidstrom, M.E.  
 J. Bacteriol. 176, 4073-4080, 1994  
 A/Title: Organization of the methyamine utilization (man) genes in Methylophilus methylotrophus  
 A/Reference number: Z16936; PMID:9422427; PMID:8021188  
 A/Accession: T10077  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-8 <CHI>  
 A/Cross-references: EMBL:U26407; NID:G561931; PID:AA646955.1; PID:G561933  
 A/Experimental source: strain W3A1  
 C/Genetic: A/Gene: manN

Query Match 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 20.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXV 5  
 : : :  
 Db 4 LQAIL 8

## RESULT 13

S68802  
 nitrate reductase (NADH) inhibitor - spinach (fragment)  
 C/Species: Spinacia oleracea (spinach)  
 C/Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998  
 C/Accession: S68802  
 R/Bachmann, M.; Huber, J.L.; Liao, P.C.; Gage, D.A.; Huber, S.C.  
 FEBS Lett. 387, 127-133, 1996  
 A/Title: The inhibitor protein of phosphorylated nitrate reductase from spinach (Spinach)  
 A/Reference number: S68802; PMID:96244508; PMID:8674533  
 A/Accession: S68802  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-8 <BAC>  
 A/Experimental source: leaves; strain cv. Bloomsdale

Query Match 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 20.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7  
 : : :  
 Db 3 LSVAY 7

## RESULT 14

PQ0726  
 unidentified 4.5/45K (imported) - rice (fragment)  
 C/Species: Oryza sativa (rice)  
 C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C/Accession: PQ0726  
 R/Komatsu, S.; Kajiwara, H.; Hiyano, H.  
 Theor. Appl. Genet. 86, 935-942, 1993  
 A/Title: A rice protein library; a data-file of rice proteins separated by two-dimensional  
 A/Reference number: PQ0696  
 A/Accession: PQ0726  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-8 <KOM>

Query Match 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 XXXVX 6  
 :|:::  
 Db 2 VQDDAA 7

## RESULT 15

JS0316  
 leucokinin VI - Madeira cockroach  
 C:Species: Leucophaea maderae (Madeira cockroach)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C:Accession: JS0316  
 R:Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 27-30, 1987  
 A:Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic  
 A:Reference number: JS0315  
 A:Accession: JS0316  
 A:Molecule type: protein  
 A:Residues: 1-8 <HOL>  
 C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act  
 C:Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (Gly) #status experimental

## Query Match

Best Local Similarity 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7  
 :|:  
 Db 4 FH 5

## RESULT 16

B45800  
 serum albumin - dog (fragment)  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 31-Dec-1993  
 C:Accession: B45800  
 R:Carraway, R.E.; Cochran, D.E.; Boucher, W.; Mitra, S.P.  
 J. Immunol. 143, 1680-1684, 1989  
 A:Title: Structures of histamine-releasing peptides formed by the action of acid proteas  
 A:Reference number: A45800; PMID:89341406; PMID:2474609  
 A:Accession: B45800  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <CAR>

## Query Match

Best Local Similarity 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7  
 :|:  
 Db 4 RH 5

## RESULT 17

A54823  
 olfactory receptor I7 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 17-Mar-1999  
 C:Accession: A54823  
 R:Chess, A.; Simon, I.; Cedar, H.; Axel, R.  
 Cell 78, 823-834, 1994  
 A:Title: Allelic inactivation regulates olfactory receptor gene expression.  
 A:Reference number: A54823; PMID:94373818; PMID:8087849  
 A:Accession: A54823  
 A:Status: preliminary  
 A:Molecule type: DNA

A:Residues: 1-8 <CHE>

Query Match 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7  
 :|:  
 Db 5 NH 6

## RESULT 18

B54823  
 olfactory receptor I7 - western wild mouse (fragment)  
 C:Species: Mus spretus (western wild mouse)  
 C:Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 17-Mar-1999  
 C:Accession: B54823  
 R:Chess, A.; Simon, I.; Cedar, H.; Axel, R.  
 Cell 78, 823-834, 1994  
 A:Title: Allelic inactivation regulates olfactory receptor gene expression.  
 A:Reference number: A54823; PMID:94373818; PMID:8087849  
 A:Accession: B54823  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-8 <CHE>

## Query Match

Best Local Similarity 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7  
 :|:  
 Db 5 NH 6

## RESULT 19

S65381  
 cytochrome-c oxidase (EC 1.9.3.1) chain VIB, hepatic - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
 C:Accession: S65381  
 R:Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.  
 Eur. J. Biochem. 230, 235-241, 1995  
 A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-termi  
 A:Reference number: S65372; PMID:95324529; PMID:7601105  
 A:Accession: S65381  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Molecule type: protein  
 A:Residues: 1-8 <SCH>  
 C:Keywords: oxidoreductase

## Query Match

Best Local Similarity 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVX 6  
 :|:::  
 Db 1 QNXLD 5

## RESULT 20

S69165  
 ferredoxin a2 - Japanese radish (fragment)  
 C:Species: Kaiware daikon (Japanese radish)  
 C:Date: 10-Mar-1998 #sequence\_revision 10-Mar-1998 #text\_change 17-Apr-1998  
 C:Accession: S69165  
 R:Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.  
 Arch. Biochem. Biophys. 316, 797-802, 1995  
 A:Title: Four ferredoxins from Japanese radish leaves.  
 A:Reference number: S69164; PMID:95168867; PMID:7864635  
 A:Accession: S69165  
 A:Molecule type: protein  
 A:Residues: 1-8 <OBA>



C:Keywords: 2pe-2s; electron transfer; iron-sulfur protein

Query Match

Best Local Similarity 36.0%; Score 9; DB 2; Length 8;

Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXV 5

DB 4 EDDIV 8

RESULT 21

A:Accession: A25836

C:Species: Escherichia coli

C>Date: 24-Jan-1988 #sequence\_revision 24-Jan-1988 #text\_change 21-Jun-2002

C:Accession: A25836

R:Heinicz, M.C.; McFall, E.

J. Bacteriol. 123, 1163-1168, 1975

A:Title: N-terminal amino acid sequences of D-serine deaminases of wild-type and operat

A:Reference number: A25836; PMID:76005414; PMID:1029073

A:Contents: K12

A:Accession: A25836

A:Molecule type: protein

A:Residues: 1-8 <HEI>

C:Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; seri

Query Match

Best Local Similarity 36.0%; Score 9; DB 2; Length 8;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7

DB 6 RH 7

RESULT 22

A:Accession: B24749

C:Species: Bos primigenius taurus (cattle)

C>Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Aug-2000

C:Accession: B24749

R:Yang, H.Y.T.; Fracta, W.; Majane, E.A.; Costa, E.

A:Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b

A:Reference number: A94074; PMID:86057985; PMID:3865193

A:Molecule type: protein

A:Residues: 1-8 <YAN>

C:Superfamily: unassigned animal peptides

C:Keywords: neuropeptide

Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4

DB 3 FQPO 6

RESULT 23

A:Accession: S19288

C:Species: Kluyvera cryocrescens

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C:Accession: S19288

R:Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Vidner, R.

Biochem. J. 280, 659-662, 1991

A:Title: Chemical modification of serine at the active site of penicillin acylase from K

A:Reference number: S19288; PMID:92109664; PMID:1764029

A:Accession: S19288

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <MAR>

Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;

Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXV 6

DB 1 CNMVI 6

RESULT 24

A:Accession: S70727

C:Species: Shigella flexneri (fragment)

C>Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 08-Oct-1999

C:Accession: S70727

R:Aliaoui, A.; Sansonetti, P.J.; Menard, R.; Barzu, S.; Mounier, J.; Phalipon, A.; Parsot

Mol. Microbiol. 17, 461-470, 1995

A:Title: Wt1g, a membrane protein required for secretion of Shigella spp. Ipa invasins: j

A:Reference number: S70727; PMID:96100445; PMID:8559055

A:Accession: S70727

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-8 <ALU>

A:Cross-references: EMBL:Z48957; NID:9929880; PIDN:CA88821.1; PID:9929881

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995

C:Genetics:

A:Gene: ipgF

Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4

DB 2 KONN 5

RESULT 25

A:Accession: S63493

C:Species: Desulfovibrio desulfuricans

C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C:Accession: S63493; S63494

R:Staubert, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.

Eur. J. Biochem. 233, 873-879, 1995

A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio c

A:Reference number: S63489; PMID:96085152; PMID:8521853

A:Accession: S63493

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <ST2>

Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;

Matches 0; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7

DB 1 ABITY 5

RESULT 26

A:Accession: PA0035

C:Species: Arabidopsis thaliana (fragment)

C>Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997

C/Accession: PA0035  
 R/Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
 Submitted to JIPD, July 1994  
 A/Description: Separation and characterization of Arabidopsis proteins by two-dimensional  
 A/Reference number: PA0001  
 A/Accession: PA0035  
 A/Molecule type: protein  
 A/Residues: 1-8 <KAM>  
 A/Experimental source: stem

Query Match 32.0%; Score 8; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 XQXX 4  
 : ||:  
 Db 1 LQXD 4

RESULT 27  
 T10952  
 hypothetical protein 1 - spring vetch  
 C/Species: Vicia sativa (spring vetch, tare)  
 C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 C/Accession: T10952  
 R/Christiansen, A.; Hansen, A.C.; Vijn, I.; Pallisgard, N.; Larsen, K.; Yang, W.C.; Blais  
 submitted to the EMBL Data Library, December 1995  
 A/Description: A novel type of DNA binding protein interacts with a conserved sequence  
 A/Reference number: Z17228  
 A/Accession: T10952  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-8 <CHR>  
 A/Cross-references: EMBL:X95995; NID:G1360633; PID:e225824

Query Match 32.0%; Score 8; DB 2; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 XQXXVX 6  
 : ||:  
 Db 2 MMTLVS 7

RESULT 28  
 S78036  
 ribosomal protein Yms-B, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)  
 C/Species: Saccharomyces cerevisiae  
 C/Date: 09-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 14-Nov-1997  
 C/Accession: S78036  
 R/Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wiltma  
 Eur. J. Biochem. 245, 449-456, 1997  
 A/Title: Identification and characterization of the genes for mitochondrial ribosomal pr  
 A/Reference number: S78018; MUID:97296414; PMID:9151978  
 A/Accession: S78036  
 A/Molecule type: protein  
 A/Residues: 1-8 <KIT>  
 A/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 32.0%; Score 8; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 XQXXVX 6  
 : ||:  
 Db 1 MNXXVD 6

RESULT 29  
 PT0030  
 inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)  
 N/Alternate names: inulase  
 C/Species: Aspergillus ficuum

C/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 07-May-1999  
 C/Accession: PT0030  
 R/Ettalibi, M.; Baratti, J.C.  
 Agric. Biol. Chem. 54, 61-68, 1990  
 A/Title: Molecular and kinetic properties of Aspergillus ficuum inulinases.  
 A/Reference number: PT0030; MUID:90344234; PMID:1368526  
 A/Accession: PT0030  
 A/Molecule type: protein  
 A/Residues: 1-8 <ETT>  
 A/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 32.0%; Score 8; DB 2; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 XQXX 4  
 : ||:  
 Db 4 DQPY 7

RESULT 30  
 PL0162  
 paramyosin - northern quahog (fragment)  
 C/Species: Mercenaria mercenaria (northern quahog)  
 C/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 11-May-2000  
 C/Accession: PL0162  
 R/Matabe, S.; Tsuchiya, T.; Hartshorne, D.J.  
 Comp. Biochem. Physiol. B 94, 813-821, 1989  
 A/Title: Phosphorylation of paramyosin.  
 A/Reference number: PL0162; MUID:90107385; PMID:2532591  
 A/Accession: PL0162  
 A/Molecule type: protein  
 A/Residues: 1-8 <MAT>  
 A/Experimental source: white adductor muscle  
 A/Note: the sequence is the phosphorylated tryptic peptide  
 C/Comment: This protein is thought to exist as a dimer of two subunits, termed alpha-par  
 om the carboxyl-terminal end of the molecule. Only alpha-paramyosin is phosphorylated by  
 F/5/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 32.0%; Score 8; DB 2; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 XQXXVX 6  
 : ||:  
 Db 2 RSMVS 7

RESULT 31  
 A46306  
 spasmogenic toxin PMV1 - spider (Phonetreria nigriventer) (fragment)  
 C/Species: Phonetreria nigriventer  
 C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 17-Mar-1999  
 C/Accession: A46306  
 R/Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.C  
 Toxicon 31, 377-384, 1993  
 A/Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide  
 A/Reference number: A46306; MUID:93276438; PMID:8503129  
 A/Accession: A46306  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-8 <MAR>

Query Match 32.0%; Score 8; DB 2; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 XQXX 4  
 : ||:  
 Db 5 GQST 8

## RESULT 32

A14683

aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragment)

N/Alternate names: aspartate aminotransferase, mitochondrial

C/Species: Gallus gallus (chicken)

C/Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000

C/Accession: A14683

R/Watson, K.J.; Hunziker, P.; Hughes, G.J.

FEBS Lett. 109, 98-102, 1979

A/Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.

A/Reference number: A14683; MUID:80092116; PMID:520566

A/Accession: A14683

A/Molecule type: Protein

A/Residues: 1-8 <MIL>

C/Keywords: aminotransferase; mitochondrion

## Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;  
Pred. No. 2.8e+05;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
:|:|:  
Db 5 FQPK 8

## RESULT 33

PT0298

Ig heavy chain CRD3 region (clone 5-103A) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C/Accession: PT0298

R/Wamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; MUID:91108337; PMID:1899102

A/Accession: PT0298

A/Molecule type: DNA

A/Residues: 1-8 <YAM>

A/Experimental source: B lymphocyte

C/Keywords: heterodimer; immunoglobulin

## Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;  
Pred. No. 2.8e+05;

Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVX 6  
:|:|:  
Db 1 RMIVV 5

## RESULT 34

PT0323

Ig heavy chain CRD3 region (clone J2-106B) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C/Accession: PT0323

R/Wamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; MUID:91108337; PMID:1899102

A/Accession: PT0323

A/Molecule type: DNA

A/Residues: 1-8 <YAM>

A/Experimental source: B lymphocyte

C/Keywords: heterodimer; immunoglobulin

## Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;  
Pred. No. 2.8e+05;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
:|:|:  
Db 4 GQRR 7

## RESULT 35

PN0043

phosphatidylethanol amine-binding protein - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998

C/Accession: PN0043

R/Kato, H.

Kawasaki Igkashahi 22, 245-259, 1996

A/Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro

A/Reference number: PN0041

A/Accession: PN0043

A/Molecule type: Protein

A/Residues: 1-8 <KAT>

A/Experimental source: neuroblastoma cell

C/Comment: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is blocked.

C/Keywords: Brain

## Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;  
Pred. No. 2.8e+05;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
:|:|:  
Db 3 EQLS 6

## RESULT 36

I49404

prealbumin - western wild mouse (fragment)

C/Species: Mus spretus (western wild mouse)

C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C/Accession: I49404

R/Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.

Mamm. Genome 5, 349-355, 1994

A/Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A/Reference number: I49334; MUID:94319082; PMID:8043949

A/Accession: I49404

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-8 <RES>

A/Cross-references: EMBL:U05683; NID:9497008; PIDN:AA60461.1; PID:G642825

## Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;  
Pred. No. 2.8e+05;

Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7  
:|:|:  
Db 1 AVVSN 5

## RESULT 37

C39690

neural cell adhesion molecule, cardiac splice form - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999

C/Accession: C39690

R/Reyes, A.A.; Small, S.J.; Akeson, R.

Mol. Cell. Biol. 11, 1654-1661, 1991

A/Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRN

A/Reference number: A39690; MUID:91141516; PMID:1996115

A/Accession: C39690

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar

A/Molecule type: mRNA

A/Residues: 1-8 <REY>

A/Cross-references: GB:M63970

C/Keywords: cardiac muscle; cell adhesion; heart

## Query Match

Best Local Similarity 32.0%; Score 8; DB 2; Length 8;  
Pred. No. 2.8e+05;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XQXX 4  
:|:|:  
Db 3 VQGE 6

## RESULT 38

A35180  
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 21-Mar-1996  
C/Accession: A35180  
R/Toshinaka, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Sato, M.  
J. Biol. Chem. 265, 5809-5815, 1990  
A/Title: Purification of a novel type of calcium-activated neutral protease from rat brain  
A/Reference number: A35180, MUID:90202830; PMID:2318836  
A/Accession: A35180  
A/Status: preliminary  
A/Molecule type: protease  
A/Residues: 1-8 <YOS>  
C/Keywords: hydrolase

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XQXXVX 6  
:|:|:  
Db 3 LSGVP 8

## RESULT 39

PC4372  
telomeric and tetraplex DNA binding protein qTBP42 II - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 28-Oct-1997 #sequence\_revision 28-Oct-1997 #text\_change 07-May-1999  
C/Accession: PC4372  
R/Saig, G.; Weisman-Shomer, P.; Fry, M.  
Biochem. Biophys. Res. Commun. 237, 617-623, 1997  
A/Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA  
A/Reference number: PC4371, MUID:97445086; PMID:9299414  
A/Accession: PC4372  
A/Molecule type: protein  
A/Residues: 1-8 <SAR>  
C/Comment: This protein binds either strand of the telomeric DNA as well as unimolecular  
F.3-8/Domain: RNP2 #status predicted <RNP>

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXXVX 6  
:|:|:  
Db 1 KXRVG 5

## RESULT 40

S29272  
tocopherol-binding protein, 81k - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 22-Nov-1993 #sequence\_revision 12-Apr-1996 #text\_change 12-Apr-1996  
C/Accession: S29272  
R/Nalecz, K.A.; Nalecz, M.J.; Azzi, A.  
Eur. J. Biochem. 209, 37-42, 1992  
A/Title: Isolation of tocopherol-binding proteins from the cytosol of smooth muscle A7-5  
A/Reference number: S29272; MUID:93011150; PMID:1396710  
A/Accession: S29272  
A/Molecule type: protein  
A/Residues: 1-8 <NAL>  
A/Experimental source: smooth muscle A7-5 cells

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 XQXX 4  
:|:|:  
Db 4 DQXQ 7

## RESULT 41

A61348  
red pigment-concentrating hormone - northern shrimp  
N/Alternate names: blanching hormone  
C/Species: Pandalus borealis (northern shrimp)  
C/Date: 02-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C/Accession: A61348; S07139  
R/Fernlund, P.; Josefsson, L.  
Science 177, 173-175, 1972  
A/Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.  
A/Reference number: A61348, MUID:72228738; PMID:5041363  
A/Accession: A61348  
A/Molecule type: protein  
A/Residues: 1-8 <FER1>

Biochim. Biophys. Acta 371, 304-311, 1974  
A/Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus borealis  
A/Reference number: S07139; MUID:75054965; PMID:4433569  
A/Accession: S07139  
A/Molecule type: protein  
A/Residues: 'E', 2-8 <FER2>

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C/Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pig-  
mented pigment-containing cells.  
C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic  
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F.6/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.0%; Score 7; DB 2; Length 8;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXX 4  
:|:|:  
Db 1 QLN 3

## RESULT 42

A28004  
adipokinetic hormone G - two-spotted cricket  
N/Alternate names: AKH-G  
C/Species: Gryllus bimaculatus (two-spotted cricket)  
C/Date: 30-Jun-1989 #sequence\_revision 24-Oct-1997 #text\_change 24-Oct-1997  
C/Accession: A28004  
R/Gade, G.; Rinehart, K.L.  
Biochem. Biophys. Res. Commun. 149, 908-914, 1987  
A/Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptic  
A/Reference number: A28004; MUID:88106553; PMID:3426616  
A/Accession: A28004  
A/Molecule type: protein  
A/Residues: 1-8 <GAR>

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F.6/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.0%; Score 7; DB 2; Length 8;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXX 4  
:|:|:  
Db 1 QVN 3

## RESULT 43

S08995

hypertrehalosemic hormone I - oriental cockroach

N/Alternate names: Pea-CAH-I

C/Species: Blatta orientalis (oriental cockroach)

C/Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997

C/Accession: S08995

R/Gade: G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Ectatostoma tiaratum assigned by tandem fast atom bombard

A/Reference number: S08995; PMID:90253659; PMID:2340112

A/Accession: S08995

A/Molecule type: protein

A/Residues: 1-8 &lt;GAB&gt;

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

## Query Match

28.0%; Score 7; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

DB 1 QVN 3

## RESULT 44

S08996

hypertrehalosemic hormone II - oriental cockroach

N/Alternate names: Pea-CAH-II

C/Species: Blatta orientalis (oriental cockroach)

C/Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997

C/Accession: S08996

R/Gade: G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Ectatostoma tiaratum assigned by tandem fast atom bombard

A/Reference number: S08995; PMID:90253659; PMID:2340112

A/Accession: S08996

A/Molecule type: protein

A/Residues: 1-8 &lt;GAB&gt;

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

## Query Match

28.0%; Score 7; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

DB 1 QLT 3

## RESULT 45

S10596

adipokinetic hormone - pond skimmer

C/Species: Libellula auripennis

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 14-Nov-1997

C/Accession: S10596

R/Gade: G.

Biol. Chem. Hoppe-Seyler 371, 475-483, 1990

A/Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating ho

A/Reference number: S10596; PMID:90359055; PMID:2390213

A/Accession: S10596

A/Molecule type: protein

A/Residues: 1-8 &lt;BIO&gt;

C/Comment: This peptide has both adipokinetic and hypertrehalosemic activities.

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; corpora cardica; hormone; neuropeptide; pyroglutamic

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

## Query Match

28.0%; Score 7; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

DB 1 QVN 3

Search completed: August 19, 2004, 15:51:22  
Job time : 11.5 secs

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OM protein - protein search, using sw model

Run on: August 19, 2004, 15:47:57 ; Search time 8 Seconds

(without alignments)  
52.070 Million cell updates/sec

Title: VARIANT2

Perfect score: 25

Sequence: 1 XQXVXHI 8

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	52.0	8	1 ACI_THUHL	P18691 thunnus alb
2	12	48.0	8	1 FUSO_FUSO	P81010 fusarium so
3	10	40.0	8	1 ANG2_BORJA	Q10582 bothrops ja
4	10	40.0	8	1 UPAL_HUMAN	P30087 homo sapien
5	9	36.0	8	1 ALIL_CYPPO	P82152 cydia pomon
6	9	36.0	8	1 COXG_RAT	P80430 rattus norv
7	9	36.0	8	1 GLUR_HUMAN	P02729 homo sapien
8	9	36.0	8	1 LCK4_LEUMA	P21143 leucophaea
9	9	36.0	8	1 LCK6_LEUMA	P19988 leucophaea
10	8	32.0	8	1 ACT_CARMA	P80709 carcinus ma
11	8	32.0	8	1 ALI7_CARMA	P81820 carcinus ma
12	8	32.0	8	1 B44K_FORGI	P81866 porphyromon
13	8	32.0	8	1 CLP_THICU	P80488 chlobacilli
14	8	32.0	8	1 CPDI_ENTFA	P13269 enterococcu
15	8	32.0	8	1 LCK3_LEUMA	P21142 leucophaea
16	8	32.0	8	1 NPMB_BOVIN	P15507 bos taurus
17	8	32.0	8	1 UC26_MAIZE	P80632 zea mays (m
18	8	32.0	8	1 UF06_MOUSE	P56575 rattus norv
19	8	32.0	8	1 UH09_RAT	P56575 rattus norv
20	7	28.0	8	1 AKHG_GRYBI	P40868 gryllus bim
21	7	28.0	8	1 AKH_LIBAU	P25418 libellula a
22	7	28.0	8	1 AKH_MEML	P25423 melolontha
23	7	28.0	8	1 AKH_TABAT	P14555 tabanus atr
24	7	28.0	8	1 CADI_ENTFA	P13268 enterococcu
25	7	28.0	8	1 COM2_CONPU	P58785 conus purpu
26	7	28.0	8	1 HTF1_PERRAM	P45458 periplaneta
27	7	28.0	8	1 HTF2_PERRAM	P45459 periplaneta
28	7	28.0	8	1 HTP_TENNO	P25419 tenebrio mo
29	7	28.0	8	1 LPK_LEUMA	P13309 leucophaea
30	7	28.0	8	1 PLP_BRANA	P81707 brassica na
31	7	28.0	8	1 RPCH_PANBO	P80893 pandalis bo
32	7	28.0	8	1 VGLG_HSV2B	P81760 herpes simp
33	6	24.0	8	1 FARI_PENVO	P83316 penaeus mon

34	6	24.0	8	1 FAR2_MACRS	P83275 macrobrachi
35	6	24.0	8	1 FAR3_HOMAM	P41486 homarus ame
36	6	24.0	8	1 FAR4_HOMAM	P41487 homarus ame
37	6	24.0	8	1 FAR7_ASCSU	P43171 ascaris suu
38	6	24.0	8	1 NSJ_MYCTU	P81152 mycobacteri
39	6	24.0	8	1 PPK3_PERRAM	P82618 periplaneta
40	6	24.0	8	1 RT34_BOVIN	P82929 bos taurus
41	5	20.0	8	1 ALI6_CYPPO	P82157 cydia pomon
42	5	20.0	8	1 CCKN_MACEU	P30369 macroopus eu
43	5	20.0	8	1 FAR4_MACRS	P83277 macrobrachi
44	5	20.0	8	1 FAR8_CALVO	P41863 calliphora
45	5	20.0	8	1 LMT2_LOCM1	P22396 locusta mig

## ALIGNMENTS

RESULT 1	ACI_THUHL	STANDARD;	PRT;	8 AA.
AC	P18691			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	01-NOV-1990 (Rel. 16, Last annotation update)			
DE	Angiotensin-converting enzyme inhibitor.			
OS	Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Euteleostei;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Euteleostei;			
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;			
OC	Scombridae; Thunnus.			
RN	NCBI_TaxID=8236;			
RP	[1]			
RC	TISSUE=Muscle;			
RX	MEDLINE=88326322; PubMed=3415688;			
RA	Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Minura T.;			
RT	"Isolation of angiotensin-converting enzyme inhibitor from tuna muscle."			
RL	Biochem. Biophys. Res. Commun. 155:332-337(1988).			
DR	PIR; A31570; A31570.			
SQ	SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;			
Query Match	52.0%;	Score 13;	DB 1;	Length 8;
Best Local Similarity	66.7%;	Pred. No. 1.4e+05;		
Matches	2;	Conservative 1;	Mismatches 0;	Gaps 0;
QY	6 XHI 8			
Db	2 THI 4			
RESULT 2	FUSO_FUSO	STANDARD;	PRT;	8 AA.
ID	P81010			
AC	P81010			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Allergen Fus s I3596* (Fragment).			
OS	Fusarium solani (subsp. pisi) (Nectria haematococca).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.			
OX	NCBI_TaxID=70791;			
RN	[1]			
RC	SEQUENCE.			
RP	STRAIN=IARI 3596; TISSUE=Mycelium;			
RA	Verma J., Gangal S.V.;			
RL	Submitted (JUL-1997) to Swiss-Prot.			
CC	-I- ALLERGEN: Causes an allergic reaction in human.			
KW	Allergen.			
FT	NON_TER			
SQ	SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;			

Query Match 48.0%; Score 12; DB 1; Length 8;  
 Best Local Similarity 20.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7  
 : : : :  
 DB 1 TTM5H 5

## RESULT 3

ANG2\_BOTUA STANDARD; PRT; 8 AA.  
 ID Q1062;  
 AC Q1062;  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Angiotensin-like peptide II (Fragment).  
 OS Bothrops jararaca (Uroaraca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=96208932; PubMed=8829801;  
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Piacarrelli Z.P.;  
 RT "Isolation and identification of angiotensin-like peptides from the  
 RT plasma of the snake Bothrops jararaca."  
 RL Comp. Biochem. Physiol. 113B:467-473(1996).  
 CC -1- SIMILARITY: Belongs to the serpin family.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT NON TER 8 8  
 SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 40.0%; Score 10; DB 1; Length 8;  
 Best Local Similarity 20.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7  
 : : : :  
 DB 2 RYVYH 6

## RESULT 4

UPA1\_HUMAN STANDARD; PRT; 8 AA.  
 ID P30087;  
 AC P30087;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Fritiger S., Paquet N., Ravier F., Pasquall C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing."  
 RT Electrophoresis 13:707-714(1992).  
 RL -1- MICROBLANBUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 4.9, its MW is: 65 kDa.  
 DR SWISS-2DPAGE; P30087; HUMAN.  
 FT UNSTRE 1 1  
 FT NON TER 8 8  
 FT UNSTRE 8 8  
 FT NON TER 8 8

SQ SEQUENCE 8 AA; 944 MW; C01772C455B806DA CRC64;

Query Match 40.0%; Score 10; DB 1; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXVX 6  
 : : : :  
 DB 2 QESNVP 7

## RESULT 5

AL11\_CYPDO STANDARD; PRT; 8 AA.  
 ID AL11\_CYPDO  
 AC P82152;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydia pomonella (Coddling moth).  
 OS Cydia pomonella (Coddling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duvé H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily."  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8 8  
 SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 36.0%; Score 9; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7  
 : : : :  
 DB 2 PH 3

## RESULT 6

COXG\_RAT STANDARD; PRT; 8 AA.  
 ID P80430;  
 AC P80430;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIb (EC 1.9.3.1) (AED) (Fragment).  
 GN COX6B.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Mistar; TISSUE=Liver;  
 RX MEDLINE=95324529; PubMed=7601105;  
 RA Schaegeer H., Noack H., Halangk W., Brandt U., von Jagow G.;  
 RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and  
 RT amino-terminal sequences suggest identity of the fetal heart and the  
 RT adult liver isoform."  
 RL Eur. J. Biochem. 230:235-241(1995).  
 CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide  
 CC chains of cytochrome c oxidase, the terminal oxidase in  
 CC mitochondrial electron transport. This protein may be one of the  
 CC heme-binding subunits of the oxidase.  
 CC -1- CATALYTIC ACTIVITY: 4 ferriocytochrome c + O(2) = 4 ferricytochrome



CC C + 2 H(2)O.  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase VIB family.  
 DR PIR: S65381; S65381.  
 KM Oxidoreductase; Mitochondrion.  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 1039 MW; 8101E9CAA73AE456 CRC64;  
 Query Match 36.0%; Score 9; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QXXVX 6  
 Db 1 QNXLD 5

RESULT 7  
 GLUR\_HUMAN STANDARD; PRT; 8 AA.  
 AC P02729;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Urine glycopeptide.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RX MEDLINE=72062338; PubMed=512685;  
 RA Lote C.J., Weiss J.B.;  
 RT "Identification in urine of a low-molecular-weight highly polar  
 glycopeptide containing cysteinyl-galactose."  
 RL Biochem. J. 123:25P-25P(1971).  
 CC -1- FUNCTION: The identity of the glycoprotein from which this peptide  
 is derived is unknown. No physiological function has been  
 attributed. An erythrocyte membrane glycopeptide having a  
 similar structure has also been found.  
 CC PIR: A03188; XGHU0.  
 DR GO; GO:0005576; C:extracellular; NMS.  
 KM Glycoprotein.  
 FT CARBOHYD 1 1  
 SQ SEQUENCE 8 AA; 855 MW; C2D87A1F5B1EB1B CRC64;  
 Query Match 36.0%; Score 9; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 XH 7  
 Db 2 EH 3

RESULT 8  
 LCK4\_LEUMA STANDARD; PRT; 8 AA.  
 AC P21143;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Leucokinin IV (L-IV).  
 OS Leucophaea maderae (Madetia cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 NCBI\_TaxID=6988;  
 RN 11  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Primary structure and synthesis of two additional neuropeptides

RT from Leucophaea maderae: members of a new family of  
 RT Cephalomyotropicins";  
 RL Comp. Biochem. Physiol. 84C:271-276(1986).  
 CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile  
 CC activity of cockroach proctodeum (hindgut).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 KM Neuropeptide; Amidation.  
 FT MOD\_RES 8 8  
 SQ SEQUENCE 8 AA; 906 MW; DC635B1E9D5BDNA CRC64;  
 Query Match 36.0%; Score 9; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 XH 7  
 Db 4 FH 5

RESULT 9  
 LCK6\_LEUMA STANDARD; PRT; 8 AA.  
 AC P19988;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Leucokinin VI (L-VI).  
 OS Leucophaea maderae (Madetia cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 NCBI\_TaxID=6988;  
 RX MEDLINE=87052651; PubMed=287794;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:  
 myotropic peptides of Leucophaea maderae."  
 RL Comp. Biochem. Physiol. 88C:27-30(1987).  
 CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile  
 CC activity of cockroach proctodeum (hindgut).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 DR PIR: JS0316; JS0316.  
 KM Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1  
 SQ SEQUENCE 8 AA; 935 MW; 9D635B1E9D5A5A6 CRC64;  
 Query Match 36.0%; Score 9; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 XH 7  
 Db 4 FH 5

RESULT 10  
 ACT\_CARMA STANDARD; PRT; 8 AA.  
 AC P80709;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Actin (Fragment).  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 NCBI\_TaxID=6759;  
 RN 11  
 RP SEQUENCE.

RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,  
 RA Baghdasarian D.;  
 RT "A transalolase. An enzyme implicated in crab steroidogenesis.";  
 RL Endocrine 5:23-32(1996).  
 CC -1- FUNCTION: Actins are highly conserved proteins that are involved  
 CC in various types of cell motility and are ubiquitously expressed  
 CC in all eukaryotic cells.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:  
 CC 6.8, ITS MW IS: 46 KDa.  
 CC -1- SIMILARITY: Belongs to the actin family.  
 DR InterPro: IPR004000; Actin\_like.  
 DR PROSITE: PS00406; ACTINS\_1; PARTIAL.  
 DR PROSITE: PS00432; ACTINS\_2; PARTIAL.  
 DR PROSITE: PS01132; ACTINS\_ACT LIKE; PARTIAL.  
 KM Structural protein.  
 FT NON\_TER 1 8  
 FT SEQUENCE 8 AA; 976 MW; 1424005AB2CAABE3 CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;  
 Best Local Similarity 20.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXX 6  
 DB 1 KCPVD 5

RESULT 11  
 AL17\_CARMA STANDARD; PRT; 8 AA.  
 AC P81820;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinus maenas (Common shore crab) (Green crab).  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OK NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 KM Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 8  
 FT SEQUENCE 8 AA; 858 MW; C82879DSAB46D865 CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
 DB 2 GQXS 5

RESULT 12  
 ID B44K\_PORGI STANDARD; PRT; 8 AA.  
 AC P81886;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE 44 KDa immunogenic protein (Fragment).  
 OS Porphyromonas gingivalis (Bacteroides gingivalis).  
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
 OC Porphyromonadaceae; Porphyromonas.  
 OK NCBI\_TaxID=837;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=VEB 3492;  
 RX MEDLINE=20198497; PubMed=10731616;  
 RA Norris J.M., Love D.N.;  
 RT "Serum antibody responses of cats to soluble whole cell antigens of  
 RT feline Porphyromonas gingivalis.";  
 RL Vet. Microbiol. 73:37-49(2000).  
 CC -1- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.  
 KM Antigen.  
 FT NON\_TER 8  
 FT SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
 DB 3 YOKR 6

RESULT 13  
 CLP\_THICU STANDARD; PRT; 8 AA.  
 AC P80488;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Chemolithotroph-specific protein (Fragment).  
 OS Thiobacillus cuprinus.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Thiomonas.  
 OK NCBI\_TaxID=16860;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=DSM 5494;  
 RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;  
 RL Submitted (SEP-1995) to Swiss-Prot.  
 CC -1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED  
 CC CHEMOLITHOTROPHICALLY.  
 FT NON\_TER 8  
 FT SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
 DB 4 AQEG 7

RESULT 14  
 CPD1\_ENTFA STANDARD; PRT; 8 AA.  
 AC P13269;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone CPD1.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OK NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=85040388; PubMed=6436978;

RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,  
 RA Craig R.A., Clewell D.B.;  
 RT "Isolation and structure of bacterial sex pheromone, cpl1.",  
 RL Science 226:849-850(1984).  
 CC -1- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC BACTERIOPHAGE PLASMID PPDI.  
 KM Pheromone.  
 SQ SEQUENCE 8 AA; 913 MW; 86658729C682C729 CRC64;  
 Query Match 32.0%; Score 8; DB 1; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 Oy 3 XXVXHI 8  
 Db 1 FVWVFL 6

RESULT 15  
 LCK3 LEUMA  
 ID LCK3 LEUMA STANDARD; PRT; 8 AA.  
 AC P21172;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Leucokinin III (L-III).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neuroptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberoidea; Leucophaea.  
 OX NCBI\_TaxId=6988;  
 RN [1]  
 RP SEQUENCE AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Primary structure and synthesis of two additional neuropeptides  
 RT from Leucophaea maderae: members of a new family of  
 RT Cephalomyotropins.";  
 RL Comp. Biochem. Physiol. 84C:271-276(1986).  
 CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile  
 CC activity of cockroach proctodeum (hindgut).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 KM Neuropeptide: Amidation.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 910 MW; DC6355B449C866DA CRC64;  
 Query Match 32.0%; Score 8; DB 1; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 XQXX 4  
 Db 1 DQGF 4

RESULT 16  
 NPMB BOVIN  
 ID NPMB BOVIN STANDARD; PRT; 8 AA.  
 AC P15507;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Morphine modulating neuropeptide B.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxId=9913;  
 RN [1]  
 RP SEQUENCE AND SYNTHESIS.  
 RC TISSUE=Brain;  
 RX MEDLINE=86067985; PubMed=3865193;  
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;

RT "Isolation, sequencing, synthesis, and pharmacological  
 RT characterization of two brain neuropeptides that modulate the action  
 RT of morphine.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).  
 CC -1- FUNCTION: Modulates the action of morphine.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 DR PIR; B24749; B24749.  
 KM Neuropeptide; Amidation.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;  
 Query Match 32.0%; Score 8; DB 1; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 XQXX 4  
 Db 3 FQFQ 6

RESULT 17  
 UC26 MAIZE  
 ID UC26 MAIZE STANDARD; PRT; 8 AA.  
 AC P80632;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)  
 DE (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxId=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Toulzet P., Riccardi F., Morin C., Damerval C., Huot J.-C.,  
 RT Pernotier J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 7.0, its MW is: 57.2 kDa.  
 DR Maize-2DPAGE; P80632; COLEOPTILE.  
 FT NON\_TER 8  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;  
 Query Match 32.0%; Score 8; DB 1; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 XQXX 4  
 Db 5 DQFK 8

RESULT 18  
 UF06 MOUSE  
 ID UF06 MOUSE STANDARD; PRT; 8 AA.  
 AC P38644;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Fibroblast;

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RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Paterson R.M., Michler L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.2, its MW is: 50 kDa.
FT NON TER
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 H 7
DB 1 H 1

RESULT 19
UH09 RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN (1)
RP SEQUENCE.
RC STRAIN=Mistar; TISSUE=Heart;
RA Li X.-P., Pleisner K.-P., Scheiler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 8.9, its MW is: 42 kDa.
FT NON TER
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXX 4
DB 4 R0SP 7

RESULT 20
AKHG GRVBI STANDARD; PRT; 8 AA.
AC P14066;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokine hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxId=6999, 7007;
RN (1)
RP SEQUENCE.
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RA MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
RT of a peptide with adipokine activity from the corpora cardiaca of
RT the cricket Gryllus bimaculatus.";
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RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN (2)
RP SEQUENCE.
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilblsch C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -1- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR InterPro: IPR002047; AKH.
DR PIR: A28004; A28004.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4
DB 1 QVN 3

RESULT 21
AKH LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokine hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxId=6966;
RN (1)
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokine/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -1- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR PIR: S10596; S10596.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4
DB 1 QVN 3
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DB 1 QVN 3

RESULT 22

AKH\_MEMLT STANDARD; PRT; 8 AA.

AC P25423;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Adipokinetic hormone (AKH).

OS Melolontha melolontha (Cockchafer),  
Geotrupes stercorarius (Dor beetle), and  
Pachnoda marginata (Flower beetle).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;  
OC Scarabaeidae; Melolonthinae; Melolontha.

OX NCBI\_TaxID=7061, 7087, 7058;

RN [1]

RP SEQUENCE.

RX SPECIES=Melolontha, and G.stercorarius; TISSUE=Corpora cardiaca;  
MEDLINE=91248100; PubMed=2039445;

RA Gaede G.;

RT "A unique charged tyrosine-containing member of the adipokinetic  
hormone/red-pigment-concentrating hormone peptide family isolated and  
sequenced from two beetle species."

RL Biochem. J. 275:671-677(1991).

RN [2]

RP SEQUENCE.

RC SPECIES=E.marginalata; TISSUE=Corpora cardiaca;  
MEDLINE=92265187; PubMed=1586453;

RX Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;

RT "Primary structures of neuropeptides isolated from the corpora  
cardiaca of various cecid beetle species determined by  
pulsed-liquid phase sequencing and tandem fast atom bombardment mass  
spectrometry."

RT Biol. Chem. Hoppe-Seyler 373:133-142(1992).

RL -1- FUNCTION: This hormone, released from cells in the corpora  
cardiaca after the beginning of flight, causes release of  
diglycerides from the fat body and then stimulates the flight  
muscles to use these diglycerides as an energy source.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.

DR PIR: A58641; A58641.

DR PIR: S15422; S15422.

DR PIR: S21663; S21663.

DR InterPro: IPR002047; AKH.

DR PROSITE: PS00256; AKH; 1.

KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD RES 8 8 AMIDATION.

SO SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4  
|::|

DB 1 QLN 3

RESULT 23

AKH\_TABAT STANDARD; PRT; 8 AA.

AC P14595;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)  
(DCC I).

DE Tabanus atratus (Horse fly).

OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;  
OC Tabanus.

OX NCBI\_TaxID=7207;

RN [1]

RP SEQUENCE.

RC TISSUE=Corpora cardiaca;  
MEDLINE=90046758; PubMed=2813385;

RX Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,  
Vogel V.W., Zhang Y.-S., Hayes D.K.;

RT "Primary structure of two neuropeptide hormones with adipokinetic and  
hypotrehalosemic activity isolated from the corpora cardiaca of horse  
flies (Diptera)."

RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).

CC -1- FUNCTION: This hormone, released from cells in the corpora  
cardiaca after the beginning of flight, causes release of  
diglycerides from the fat body and then stimulates the flight  
muscles to use these diglycerides as an energy source.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.

DR PIR: A33995; A33995.

DR InterPro: IPR002047; AKH.

DR PROSITE: PS00256; AKH; 1.

KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD RES 8 8 AMIDATION.

SO SEQUENCE 8 AA; 949 MW; 8678677A9D1A736 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4  
|::|

DB 1 QLT 3

RESULT 24

CAD1\_ENTFA STANDARD; PRT; 8 AA.

AC P13266;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Sex pheromone CAD1.

OS Enterococcus faecalis (Streptococcus faecalis).

OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OX NCBI\_TaxID=1351;

RN [1]

RP SEQUENCE.

RX MEDLINE=85051889; PubMed=6437872;

RA Mori M., Sakagami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
Craig R.A., Clewell D.B., Suzuki A.;

RT "Isolation and structure of the bacterial sex pheromone, CAD1, that  
induces plasmid transfer in Streptococcus faecalis."

RL FEMS Lett. 178:97-100(1994).

CC -1- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
HEMOLYSIN PLASMID PAD1.

KW Pheromone.

SO SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;  
Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVX 6  
|::|

DB 3 SLVL 6

RESULT 25

COM2\_CONFU STANDARD; PRT; 8 AA.

AC P58785;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contrypphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxId=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=9388839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contrypphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -1- SIMILARITY: Belongs to the contrypphan family.
KM Toxin; Hydroxylation; D-amino acid.
FT DISUFID 2 8
FT MOD_RES 4 4 D-LEUCINE.
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVX 6
Db 1 GCVL 4

RESULT 26
HTF1_PERAM STANDARD; PRT; 8 AA.
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-1)
DE (Pea-CAH-I) (Led-CC-I) (Hypertrehalosaemic neuropeptide I).
OS Periplaneta americana (American cockroach),
OS Lepitornata decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxId=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548629;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.

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RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Grylmodorina portenlosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph of insects.
CC the major carbohydrate in the hemolymph of insects.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR PIR; A05169; A05169.
DR PIR; A44960; A44960.
DR PIR; A49823; A49823.
DR PIR; S08995; S08995.
DR InterPro; IPR02047; AKH.
DR PROSITE; PS00256; AKH; 1.
KM Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QXX 4
Db 1 QVN 3

RESULT 27
HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplanetin CC-2)
DE (Pea-CAH-II) (Led-CC-II) (Hypertrehalosaemic neuropeptide II).
OS Periplaneta americana (American cockroach),
OS Lepitornata decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxId=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;

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RT "Isolation and primary structure of two peptides with  
RT cardiocellulose and hypertrichalose activity from the corpora  
RT Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).  
RN [1]  
RP SPECIES=L.deceimlineata; TISSUE=Corpora cardiaca;  
RX MEDLINE=90160053; Pubmed=2576128;  
RA Gaede G., Kellner R.;  
RT "The metabolic neuropeptides of the corpus cardiaca from the potato  
RT beetle and the American cockroach are identical.";  
RL Peptides 10:1287-1289(1989).  
RN [4]  
RP SPECIES=B.orientalis; TISSUE=Corpora cardiaca;  
RX MEDLINE=90253659; Pubmed=2340112;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary structures of hypertrichalose and neuropeptides isolated from  
RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
RT Gromphadorhina portenosa, Blattella germanica and Blatta orientalis  
RT and of the stick insect Extracostoma titatum assigned by tandem fast  
RT atom bombardment mass spectrometry.";  
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
CC -1- FUNCTION: Hypertrichalose and neuropeptides that  
CC elevate the level of trehalose in the hemolymph (trehalose is the  
CC major carbohydrate in the hemolymph of insects).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the AKH / HRTM / RPCH family.  
DR PIR; B44960; B44960.  
DR PIR; B49823; B49823.  
DR PIR; S08996; S08996.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
DR Neuropeptide; Amidation; Pyroglutamate carboxylic acid.  
KM MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9DA736 CRC64;  
Query Match 28.0%; Score 7; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 2 QXX 4  
DB 1 QLT 3  
RESULT 28  
HTF TENMO STANDARD; PRT; 8 AA.  
ID HTF TENMO  
AC P25419;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypertrichalose factor (HOTH) (Hypertrichalose neuropeptide).  
OS Tenebrio molitor (Yellow mealworm), and  
OS Zophobas rugipes.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
OC Tenebrionidae; Tenebrio.  
OX NCBI\_Taxid=7067, 7075;  
RN [1]  
RP SPECIES=T.molitor, and Z.rugipes;  
RX TISSUE=Corpora cardiaca;  
MEDLINE=90341081; Pubmed=3381871;  
RA Gaede G., Rosinski G.;  
RT "The primary structure of the hypertrichalose neuropeptide from  
RT tenebrionid beetles: a novel member of the AKH/RPCH family.";  
RL Peptides 11:455-459(1990).  
CC -1- FUNCTION: Hypertrichalose and neuropeptides that  
CC elevate the level of trehalose in the hemolymph (trehalose is the  
CC major carbohydrate in the hemolymph of insects).

CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the AKH / HRTM / RPCH family.  
DR PIR; A43976; A43976.  
DR PIR; B43976; B43976.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KM Neuropeptide; Amidation; Pyroglutamate carboxylic acid.  
FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;  
Query Match 28.0%; Score 7; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 2 QXX 4  
DB 1 QLN 3  
RESULT 29  
LPK LEUMA STANDARD; PRT; 8 AA.  
ID LPK LEUMA  
AC P13049;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Leukopyrokinin (LPK) (LBM-PK).  
OS Leucophaea maderae (Maderia cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_Taxid=6988;  
RN [1]  
RP SPECIES=L.maderae; Pubmed=3015140;  
RX MEDLINE=86269041; Pubmed=3015140;  
RA Nachman R.J., Holman G.M., Cook B.J.;  
RT "Active fragments and analogs of the insect neuropeptide  
RT Leukopyrokinin: structure-function studies.";  
RL Biochem. Biophys. Res. Commun. 137:936-942(1986).  
RN [2]  
RP SPECIES=L.maderae; Pubmed=2877794;  
RX MEDLINE=87052651; Pubmed=2877794;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Primary structure and synthesis of a blocked myotropic  
RT neuropeptide isolated from the cockroach, Leucophaea maderae.";  
RL Comp. Biochem. Physiol. 85C:219-224(1986).  
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
CC activity).  
CC -1- MISCELLANEOUS: An analog without the N-terminal PCA residue was  
CC synthesized and found to exhibit greater activity (1448) than the  
CC parent neuropeptide. The portion of the sequence of LPK most  
CC critical for the myotropic properties is limited to the  
CC pentapeptide fragment FPRPL.  
CC -1- SIMILARITY: Belongs to the pyrokinin family.  
DR PIR; A23967; A23967.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KM Neuropeptide; Amidation; Pyrokinin; Pyroglutamate carboxylic acid.  
FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;  
Query Match 28.0%; Score 7; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 2 QXX 4  
DB 1 QTS 3

RESULT 30  
 PLE\_BRANA STANDARD; PRT; 8 AA.  
 AC P81707;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Placidal lipid-associated protein (Fragment).  
 OS Brassica napus (Rape).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Euphorbia; Brassicales; Brassicaceae; Brassica.  
 NC NCB1\_TaxID=706;  
 RN (1)  
 RP SEQUENCE.  
 RC STRAIN=CV. TOPAZ; TISSUE=Tapetum;  
 RX MEDLINE=99349136; PubMed=10420651;  
 RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,  
 RA Murphy D.J.,  
 RT "Composition and role of tapetal lipid bodies in the biogenesis of the  
 RT pollen coat of Brassica napus."  
 RL Planta 208:588-598(1999).  
 CC -1- FUNCTION: May play a structural role in the elaioplast, a tapetum-  
 CC specific placidal lipid organelle.  
 CC -1- TISSUE SPECIFICITY: Tapetum of anthers.  
 CC NON TER  
 FT SEQUENCE 8 AA; 989 MW; 9D7B1A452CA042 CRC64;  
 SQ

Query Match 28.0%; Score 7; DB 1; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 VXXI 8  
 |:::  
 Db 1 VIDV 4

RESULT 31  
 RPCH\_PANBO STANDARD; PRT; 8 AA.  
 ID RPCH\_PANBO  
 AC P08939;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Red pigment concentrating hormone (RPHC).  
 OS Pandanus borealis (Northern red shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidae;  
 OC Pandalidae; Pandalus.  
 NC NCB1\_TaxID=6703;  
 RN (1)  
 RP SEQUENCE.  
 RX MEDLINE=75054965; PubMed=4433569;  
 RA Fernlund P.,  
 RT "Structure of the red-pigment-concentrating hormone of the shrimp,  
 RT Pandanus borealis."  
 RL Biochim. Biophys. Acta 371:304-311(1974).  
 CC -1- FUNCTION: This hormone adapts the animal to light backgrounds by  
 CC stimulating concentration of the pigment of its red body-  
 CC chromatophores.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
 DR InterPro: IPR002047; AKH.  
 DR PROSITE: PS00256; AKH; 1.  
 KW pigment; Hormone; Amidation; Pyroglutamate carboxylic acid.  
 FT MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD RES 8 8 AMIDATION.  
 FT SEQUENCE 8 AA; 948 MW; 8678675B9C44736 CRC64;  
 SQ

Query Match 28.0%; Score 7; DB 1; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QXX 4  
 |:::  
 Db 1 QLN 3  
 RESULT 32  
 VGLG\_HSV2B STANDARD; PRT; 8 AA.  
 ID VGLG\_HSV2B  
 AC P81780;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Glycoprotein G (Fragment).  
 OS Herpes simplex virus (type 2 / strain B43270R).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 NC NCB1\_TaxID=103921;  
 RN (1)  
 RP SEQUENCE.  
 RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.,  
 RL Submitted (APR-1999) to Swiss-Prot.  
 CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND  
 CC 2: GH, GB, GC, GD, GI, AND GE.  
 CC -1- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN  
 CC HSV-1.  
 CC Glycoprotein.  
 KW NON TER  
 FT SEQUENCE 8 AA; 683 MW; 7B47686772C865B8 CRC64;  
 SQ

Query Match 28.0%; Score 7; DB 1; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVX 6  
 |:::  
 Db 2 SGVP 5

RESULT 33  
 FAR1\_PENMO STANDARD; PRT; 8 AA.  
 ID FAR1\_PENMO  
 AC P83316;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide Flrp1 (GDRNF1LR-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 NC NCB1\_TaxID=6687;  
 RN (1)  
 RP SEQUENCE AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupum J., Krungkarn S.,  
 RA Chaivisuthangkura P., Sithigorngul W., Peterson A.,  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 RT of the giant tiger prawn Penaeus monodon."  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 DR GO: GO:0007218; P-neuropeptide signaling pathway; TAS.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8 8 AMIDATION.  
 FT SEQUENCE 8 AA; 1024 MW; 72D40729CA540AA8 CRC64;  
 SQ

Query Match 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;



QY 1 XQXXVX 6 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

RESULT 34  
 FAR2\_MACRS STANDARD; PRT; 8 AA.

AC P31275;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE FMRamide-like neuropeptide FLP2 (ADKNFLRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_Taxid=79674;  
 RN [1]  
 RP SEQUENCE. AND MASS SPECTROMETRY.  
 RC TISSUE=Dorsal; Sarathongkum W., Jaidechoe S., Longyant S.,  
 RA Sthigorngul P.,  
 RA Sthigorngul W.,  
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii.";  
 RL Comp. Biochem. Physiol. 120B:587-595 (1998).  
 CC -1- MASS SPECTROMETRY: MW=1009.4, METHOD=MALDI.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 DR GO:0007218; P:neuropeptide signaling pathway; TMS.  
 KM Neuropeptide; Amidation.  
 FT MOD RES 8  
 SO SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6  
 Db 2 DKNFLR 7

RESULT 35  
 FAR3\_HOMAM STANDARD; PRT; 8 AA.

AC P41486;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DE FMRamide-like neuropeptide 3 (FLI 3) (F2).  
 OS Homarus americanus (American lobster).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Ascaridea;  
 OC Nephropoidea; Nephropidae; Homarus.  
 OX NCBI\_Taxid=6706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=8811614; PubMed=3429714;  
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.,  
 RT "Purification and characterization of FMRamide-like immunoreactive  
 RT substances from the lobster nervous system: Isolation and sequence  
 RT analysis of two closely related peptides.";  
 RL J. Comp. Neurol. 266:16-26 (1987).  
 CC -1- MISCELLANEOUS: Pericardial organs release this peptide with 100 mM  
 CC potassium in the presence of calcium.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 KM Neuropeptide; Amidation.  
 FT MOD RES 8  
 SO SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6  
 Db 2 DKNFLR 7

RESULT 36  
 FAR4\_HOMAM STANDARD; PRT; 8 AA.

AC P41487;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DE FMRamide-like neuropeptide 4 (FLI 4) (F1).  
 OS Homarus americanus (American lobster).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Ascaridea;  
 OC Nephropoidea; Nephropidae; Homarus.  
 OX NCBI\_Taxid=6706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=8811614; PubMed=3429714;  
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.,  
 RT "Purification and characterization of FMRamide-like immunoreactive  
 RT substances from the lobster nervous system: Isolation and sequence  
 RT analysis of two closely related peptides.";  
 RL J. Comp. Neurol. 266:16-26 (1987).  
 CC -1- FUNCTION: Can act as a modulator of exoskeletal and cardiac  
 CC neuromuscular junctions.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 KM Neuropeptide; Amidation.  
 FT MOD RES 8  
 SO SEQUENCE 8 AA; 1067 MW; DDD40729C4540A51 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6  
 Db 2 DKNFLR 7

RESULT 37  
 FAR7\_ASCSU STANDARD; PRT; 8 AA.

AC P41471;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DE FMRamide-like neuropeptide AF7.  
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;  
 OC Ascaridoidea; Ascaris.  
 OX NCBI\_Taxid=6253;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95380362; PubMed=7651904;  
 RA Cowden C., Stretton A.O.W.,  
 RT "Eight novel FMRamide-like neuropeptides isolated from the nematode  
 RT Ascaris suum.";  
 RL Peptides 16:491-500 (1995).  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 KM Neuropeptide; Amidation.  
 FT MOD RES 8  
 SO SEQUENCE 8 AA; 963 MW; 9CD40059D417687D CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVX 6  
 DB 4 RFLR 7

RESULT 38  
 NS3\_MYCTU STANDARD; PRT; 8 AA.

AC P81152;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 30 kDa non-secretory protein 3 (Fragment).  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinomycetales;  
 OC Corynebacteriaceae; Mycobacterium.  
 OC NCBI\_TaxID=1773;  
 RN (1)  
 RP SEQUENCE.  
 RC STRAIN=H37Rv;  
 RA Prasad H.K., Annapurna P.S.;  
 RL Submitted (DEC-1997) to Swiss-Prot.  
 CC -1- CAUTION: We are unable to find this protein in the translation of  
 the genome of strain H37Rv.  
 FT NON\_TER 1 8  
 FT NON\_TER 1 8  
 SQ SEQUENCE 8 AA; 919 MW; 8D3DC40B19CDD2D2 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 XXVX 6  
 DB 1 VVA 3

RESULT 39  
 PPK3\_PERAM STANDARD; PRT; 8 AA.  
 AC P82618;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-3 (Pea-PK-3) (FXPRU-amide).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;  
 OC Blattidae; Periplaneta.  
 OC NCBI\_TaxID=6978;  
 RN (1)  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Retrocerebral complex;  
 RX MEDLINE=99212469; PubMed=10196736;  
 RA Predel R., Kellner R., Nechman R.J., Holman G.M., Rapus J., Gaede G.;  
 RT "Differential distribution of pyrokinin-isoforms in cerebral and  
 abdominal neuromal organs of the American cockroach.";  
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).  
 RN (2)  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRUamides in the nervous system of  
 the American cockroach.";  
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
 activity).  
 CC -1- TISSUE SPECIFICITY: Corpora cardiaca.

CC -1- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.  
 CC -1- SIMILARITY: Belongs to the pyrokinin family.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 8 8  
 FT MOD\_RES 8 8  
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 XXVX 6  
 DB 1 LVP 3

RESULT 40  
 RT34\_BOVIN STANDARD; PRT; 8 AA.

AC P82929;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).  
 GN MRPS34.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN (1)  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=21276436; PubMed=11279123;  
 RA Koc B.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.;  
 RT "The small subunit of the mammalian mitochondrial ribosome:  
 identification of the full complement of ribosomal proteins present.";  
 RL J. Biol. Chem. 276:19363-19374(2001).  
 CC -1- SUBUNIT: Component of the mitochondrial ribosome small subunit  
 (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 KW Ribosomal protein; Mitochondrion.  
 FT NON\_TER 1 1  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVX 6  
 DB 2 WGI 5

RESULT 41  
 ALL6\_CYDPO STANDARD; PRT; 8 AA.  
 AC P82157;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydia pomonella (Codling moth).  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OC NCBI\_TaxID=82600;  
 RN (1)  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Dive H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 Davey M., East P.D., Thorpe A.;

RT "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 KM Neuropeptide; Amidation.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 936 MW; 082879C45B573767 CRC64;  
 Query Match 20.0%; Score 5; DB 1; Length 8;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7  
 Db 1 LPLYN 5

RESULT 42  
 CCKN\_MACEU STANDARD; PRT; 8 AA.  
 ID CCKN\_MACEU  
 AC P30369;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Cholecystokinin (CCK).  
 GN CCK.  
 OS Macropus eugenii (Tamar wallaby), and  
 OS Dasypus viverrinus (Southeastern quoll).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.  
 OX NCBI\_TaxID=9315, 9279;  
 RX MEDLINE=88234141; PubMed=3375140;  
 RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;  
 RT "Cholecystokinin octapeptide purified from brains of Australian  
 RT marsupials";  
 RL Peptides 9:429-431(1988).  
 CC -1- FUNCTION: This peptide hormone induces gall bladder contraction  
 CC and the release of pancreatic enzymes in the gut. Its function in  
 CC the brain is not clear.  
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR PIR; P00012; P00012.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 KM Amidation; Sulfation; Hormone.  
 FT MOD RES 2  
 FT MOD RES 8  
 FT MOD RES 2  
 SQ SEQUENCE 8 AA; 1064 MW; DDCA68378768B5A CRC64;  
 Query Match 20.0%; Score 5; DB 1; Length 8;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVX 6  
 Db 2 YMGWMD 7

RESULT 43  
 PAR4\_MACRS STANDARD; PRT; 8 AA.  
 ID PAR4\_MACRS  
 AC P83277;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide PUP4 (APALRIP-amide).  
 OS Macrobrachium rosenbergii (Giant Fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Placodymata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.

OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Bystrak.  
 RA Stihgornigul P., Sarathongkum W., Jaidechoe S., Longyant S.,  
 RA Stihgornigul W.;  
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii.";  
 RL Comp. Biochem. Physiol. 120B:587-595 (1998).  
 CC -1- MASS SPECTROMETRY: MW=943; METHOD=MALDI.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 CC GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
 DR Neuropeptide; Amidation.  
 FT MOD RES 8  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 943 MW; 9CD40734072DC76D CRC64;  
 Query Match 20.0%; Score 5; DB 1; Length 8;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 XXVXH 8  
 Db 1 APALRL 6

RESULT 44  
 FARP\_CALVO STANDARD; PRT; 8 AA.  
 ID FARP\_CALVO  
 AC P41863;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliphora vomitoria (Blue blowfly).  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Thoracic ganglion;  
 RX MEDLINE=9219611; PubMed=1549595;  
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliphorin) from the blowfly  
 RT Calliphora vomitoria";  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.  
 CC PIR; H41978; H41978.  
 DR Neuropeptide; Amidation.  
 FT MOD RES 8  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 957 MW; 72D4069C4A44DD8 CRC64;  
 Query Match 20.0%; Score 5; DB 1; Length 8;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVX 6  
 Db 2 ANDPMR 7

RESULT 45  
 LMT2\_LOCM1 STANDARD; PRT; 8 AA.  
 ID LMT2\_LOCM1  
 AC P22356;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-AUG-1991 (Rel. 19, Last annotation update)  
 DE Locustamytotropin 2 (LOM-MT-2).

OS Locusta migratoria (migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
RT "Isolation, identification and synthesis of locustamyotropin II, an  
RT additional neuropeptide of Locusta migratoria. Member of the  
RT cephalomyotropic peptide family.";  
RL Insect Biochem. 20:479-484(1990).  
CC -I- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
CC activity).  
CC -I- SIMILARITY: Belongs to the pyrokinin family.  
DR InterPro: IPR001484; Pyrokinin.  
DR PROSITE: PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 8 AMIDATION.  
SQ SEQUENCE 8 AA; 934 MW; 2634171A9CNA87B CRC64;

Query Match 20.0%; Score 5; DB 1; Length 8;  
Best Local Similarity 0.0%; Pred. NO. 1.4e+05;  
Matches 0; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 XXVXHI 8  
   :::;  
DB 3 DFTPRL 8

Search completed: August 19, 2004, 15:51:49  
Job time : 9 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 19, 2004, 15:47:57 / Search time 31 Seconds  
(without alignments)  
81.424 Million cell updates/sec

Title: VARIANT2  
Perfect score: 25  
Sequence: 1 XQXVXHI 8

Scoring table: BLOSUM62DX  
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 414

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	60.0	8	4	Q7Z6G0
2	14	56.0	8	2	Q56246
3	14	56.0	8	9	Q37854
4	14	56.0	8	13	Q91098
5	14	56.0	8	13	Q90498
6	13	52.0	8	2	P72279
7	13	52.0	8	2	P83152
8	12	48.0	8	5	Q9ZEW9
9	12	48.0	8	5	Q9TWH6
10	12	48.0	8	5	Q02032
11	12	48.0	8	4	Q15894
12	11	44.0	8	4	Q15894
13	11	44.0	8	4	Q9UWC7
14	11	44.0	8	6	Q9XSY1
15	11	44.0	8	8	Q8WGC9
16	11	44.0	8	10	Q8L802

17	11	44.0	8	13	P79940	P79940 xenopus lae
18	10	40.0	8	2	Q45615	Q45615 bacillus su
19	10	40.0	8	2	Q95443	Q95443 pseudomonas
20	10	40.0	8	2	Q8G940	Q8G940 borrelia bu
21	10	40.0	8	3	Q05403	Q05403 saccharomyc
22	10	40.0	8	3	Q13591	Q13591 saccharomyc
23	10	40.0	8	4	Q9BY75	Q9BY75 homo sapien
24	10	40.0	8	4	Q9UD24	Q9UD24 homo sapien
25	10	40.0	8	4	Q15893	Q15893 homo sapien
26	10	40.0	8	4	Q9UMH9	Q9UMH9 homo sapien
27	10	40.0	8	4	Q8IV87	Q8IV87 homo sapien
28	10	40.0	8	5	Q8MUN6	Q8MUN6 heliconius
29	10	40.0	8	5	Q86B59	Q86B59 strongyloce
30	10	40.0	8	6	Q9T778	Q9T778 canis fami
31	10	40.0	8	6	Q9BR82	Q9BR82 ursus arcto
32	10	40.0	8	6	Q9BRC2	Q9BRC2 macropus eu
33	10	40.0	8	6	Q9BF90	Q9BF90 trageleaphus
34	10	40.0	8	6	Q9BFB1	Q9BFB1 echinops te
35	10	40.0	8	6	Q9BFA1	Q9BFA1 ateleus fusc
36	10	40.0	8	6	Q9BR87	Q9BR87 caprine ind
37	10	40.0	8	6	Q9BFB9	Q9BFB9 euphractus
38	10	40.0	8	6	Q9BFB8	Q9BFB8 chaetophrac
39	10	40.0	8	6	Q9BFA0	Q9BFA0 macaca mula
40	10	40.0	8	6	Q9BFA8	Q9BFA8 loxodonta a
41	10	40.0	8	6	Q9BFA9	Q9BFA9 procavia ca
42	10	40.0	8	6	Q9BFB2	Q9BFB2 sorex arane
43	10	40.0	8	6	Q9BFB5	Q9BFB5 erinaceus c
44	10	40.0	8	6	Q9BFB6	Q9BFB6 myrmecophag
45	10	40.0	8	6	Q9BFB3	Q9BFB3 condylura c

## ALIGNMENTS

### RESULT 1

ID Q7Z6G0 PRELIMINARY; PRT; 8 AA.  
AC Q7Z6G0;  
DT 01-OCT-2003 (T-EMBLrel. 25, Created)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Fumarate hydratase (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wei M.-H., Nickerson M.L., Toro J.R.;  
RT "Haplotype repeat polymorphisms in the fumarate hydratase gene of  
human chromosome 14q23.3.";  
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY29638; AAB5732.1;  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 881 MW; 40CSB1E732C44330 CRC64;

Query Match 60.0%; Score 15; DB 4; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1e+06;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7  
DB 2 KNVVLH 6

### RESULT 2

ID Q56246 PRELIMINARY; PRT; 8 AA.  
AC Q56246; Q52410;  
DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)  
DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)

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DE Thermophilic proton ATPase epsilon subunit amino terminal (Fragment).
OS Thermophilic bacterium PS3.
OC Bacteria; Firmicutes; Bacillales.
OX NCB1_TaxID=2334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PS3;
RX MEDLINE=87137359; PubMed=2880841;
RA Kagawa Y., Ishizuka M., Saitou T., Nakao S.;
RL "Stable structure of thermophilic proton ATPase beta subunit.";
DR EMBL; D00113; BAA00067.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 914 MW; EBD5A2C1E041A336 CRC64;

Query Match 56.0%; Score 14; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 1e+06;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXHI 8
Db 1 MKRIHV 6

RESULT 3
Q37854 PRELIMINARY; PRT; 8 AA.
ID Q37854;
AC Q37854;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Coliphage gene of unknown function, 5' end (Fragment).
OS Bacteriophage R17.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC NCB1_TaxID=12026;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=73224987; PubMed=4352721;
RA Rensing U.F.E.;
RT "A sequence of seventy-three nucleotides from the Coliphage R17
genome.";
RL Biochem. J. 131:593-604(1973).
DR EMBL; M24820; AAA72755.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 969 MW; ECB45412C1E72726 CRC64;

Query Match 56.0%; Score 14; DB 9; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 XVXHI 8
Db 1 MLTIV 5

RESULT 4
Q91098 PRELIMINARY; PRT; 8 AA.
ID Q91098;
AC Q91098;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Myoglobin (Fragment).
OS Manotina melanocephala (Noisy miner).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Melipnagidae; Manotina.
OX NCB1_TaxID=44314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D02;
RX MEDLINE=98208049; PubMed=9548272;

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RA Heslewood M.M., Elphinstone M.S., Tidemann S.C., Beverstock P.R.;
RT "Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae
assessed by temperature gradient gel electrophoresis.";
RL Electrophoresis 19:142-151(1998).
DR EMBL; U04097; AAC60364.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 890 MW; C6C1F2C865B046DE CRC64;

Query Match 56.0%; Score 14; DB 13; Length 8;
Best Local Similarity 28.6%; Pred. No. 1e+06;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXVXH 7
Db 1 CQISGVH 7

RESULT 5
Q90498 PRELIMINARY; PRT; 8 AA.
ID Q90498;
AC Q90498;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Myoglobin (Fragment).
OS Erythrura gouldiae (Gouldian finch).
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidae; Passeridae;
OC Erythrura.
OX NCB1_TaxID=44316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGG1;
RX MEDLINE=98208049; PubMed=9548272;
RA Heslewood M.M., Elphinstone M.S., Tidemann S.C., Beverstock P.R.;
RT "Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae
assessed by temperature gradient gel electrophoresis.";
RL Electrophoresis 19:142-151(1998).
DR EMBL; U04096; AAC60363.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 890 MW; C6C1F2C865B046DE CRC64;

Query Match 56.0%; Score 14; DB 13; Length 8;
Best Local Similarity 28.6%; Pred. No. 1e+06;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXVXH 7
Db 1 CQISGVH 7

RESULT 6
P72279 PRELIMINARY; PRT; 8 AA.
ID P72279;
AC P72279;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Biphényl dioxygenase (Fragment).
OS Rhodococcus globensul.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterinae; Nocardiaceae; Rhodococcus.
OX NCB1_TaxID=33008;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95255652; PubMed=7737502;
RA Asturias J.A., Diaz E., Timmis K.N.;
RT "Evolutionary relationship of the biphényl dioxygenase of the gram-
positive bacterium Rhodococcus globensul P6 to multicomponent
dioxygenases of gram-negative bacteria.";

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RL Gene 156:11-18(1995).  
 DR EMBL; X80041; CA56350.1; -  
 DR GO: GO:0016702; P:oxidoreductase activity, acting on single d. . .; IEA.  
 KM Dioxigenase.  
 PT NON\_TER  
 SQ SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;  
 QY  
 Db 1 XQXXVX 6  
 3 LQDEVV 8  
 Query Match 52.0%; Score 13; DB 2; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1e+06;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 7  
 ID P83152 PRELIMINARY; PRT; 8 AA.  
 AC P83152;  
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)  
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE Allophycocyanin beta chain (Fragment).  
 OS Anabaena sp. (strain L31).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.  
 NC NCB1\_TaxID=29412;  
 RN [1]  
 RP SEQUENCE.  
 RA Apte S.K., Uhlemann E., Schmid R., Alendort K.;  
 RL Submitted (OCT-2001) to Swiss-Prot.  
 CC -1- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BLUE PIGMENT-PROTEIN  
 FROM THE PHYCOBILIPROTEIN COMPLEX. ALLOPHYCOCYANIN HAS A MAXIMUM  
 ABSORPTION AT APPROXIMATELY 650 TO 653 NANOMETERS.  
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
 CC -1- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE.  
 CC -1- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0030089; C:phycobilliposome; IEA.  
 DR GO: GO:0009579; C:chylakoid; IEA.  
 DR GO: GO:0006118; P:electron transport; IEA.  
 DR GO: GO:0015979; P:photosynthesis; IEA.  
 KM Phycobilliposome; Electron transport; Photosynthesis; Blue pigment;  
 KW Thylakoid; Membrane.  
 PT NON\_TER  
 SQ SEQUENCE 8 AA; 788 MW; 87CDCA05DDAB6DD CRC64;  
 Query Match 52.0%; Score 13; DB 2; Length 8;  
 Best Local Similarity 12.5%; Pred. No. 1e+06;  
 Matches 1; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 XQXXVX 8  
 Db 1 AQDAITAV 8  
 RESULT 8  
 ID Q9ZE29 PRELIMINARY; PRT; 8 AA.  
 AC Q9ZE29;  
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)  
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
 DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).  
 GN LEUA.  
 OS Buchnera aphidicola.  
 OC Bacterioidetes; Bacterioidia; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Buchnera.  
 NC NCB1\_TaxID=9;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99028904; PubMed=9812361;

RA Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;  
 RT "Structure and evolution of the leucine plasmids carried by the  
 RT endosymbiont (Buchnera aphidicola) from aphids of the family  
 RT Aphididae".  
 RL FEMS Microbiol. Lett. 168:43-49(1998).  
 DR EMBL; AU006874; CA07290.1; -  
 DR GO: GO:0046821; C:extrachromosomal DNA; IEA.  
 DR GO: GO:0003852; P:2-isopropylmalate synthase activity; IEA.  
 DR GO: GO:0016829; P:lyase activity; IEA.  
 KM lyase; Plasmid.  
 PT NON\_TER  
 SQ SEQUENCE 8 AA; 917 MW; FE205042D6C5B446 CRC64;  
 QY  
 Db 1 XQXXVX 6  
 3 SOVITL 8  
 Query Match 48.0%; Score 12; DB 2; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 1e+06;  
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 9  
 ID Q9TWH6 PRELIMINARY; PRT; 8 AA.  
 AC Q9TWH6;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)  
 DE BIOACTIVE peptide P4=PUTATIVE ESOPHAGEAL NEUROREGULATOR.  
 OS Periwinkle vancaurica.  
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;  
 OC Phyllodoctida; Nereididae; Periwinkels.  
 NC NCB1\_TaxID=6355;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=95323338; PubMed=7599979;  
 RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.,  
 RA Fujita T., Minkata H., Nomoto K.;  
 RT "Isolation and characterization of four novel bioactive peptides from  
 RT a polychaete annelid, Periwinkle vancaurica".  
 RL Comp. Biochem. Physiol. C, Pharmacol. Toxicol. Endocrinol. 110:297-  
 304(1995).  
 SQ SEQUENCE 8 AA; 989 MW; 954772CAAB780B59 CRC64;  
 Query Match 48.0%; Score 12; DB 5; Length 8;  
 Best Local Similarity 14.3%; Pred. No. 1e+06;  
 Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 XQXXVX 7  
 Db 2 YEGDVPY 8  
 RESULT 10  
 ID O02032 PRELIMINARY; PRT; 8 AA.  
 AC O02032;  
 DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
 DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
 DT 01-NOV-1998 (T-EMBLrel. 08, Last annotation update)  
 DE Metallothionein (Fragment).  
 GN LEMT2.  
 OS Lytechinus pictus (Painted sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinozoa; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinozoa; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Lytechinus.  
 NC NCB1\_TaxID=7653;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97264487; PubMed=9110313;  
 RA Caerjesi P., Fang H., Brandhorst B.P.;  
 RT "Metallothionein gene expression in embryos of the sea urchin

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RT Lytechinus pictus."
RL Mol. Reprod. Dev. 47:39-46(1997).
DR EMBL; U83400; AAB58320.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 823 MW; BBD5A2C1F7686766 CRC64;

Query Match
Best Local Similarity 48.0%; Score 12; DB 5; Length 8;
Pred. No. 1e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHV 8
DB 4 PHV 6

RESULT 11
Q34909 PRELIMINARY; PRT; 8 AA.
AC Q34909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
OS Locusta migratoria (Migratory locust).
OC Insecta; Orthoptera; Orthoptera; Acrididae; Acridomorpha;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88223478; PubMed=2836084;
RA McCracken A., Uhlenbusch I., Gellissen G.;
RT "Structure of the cloned locusta migratoria mitochondrial genome:
RT restriction mapping and sequence of its ND-1 (URF-1) gene.";
RL Curr. Genet. 11:625-630(1987).
DR EMBL; X05286; CAA28905.1; -.
KW Mitochondrion.
DR GO; GO:0005739; Mitochondrion; IEA.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match
Best Local Similarity 48.0%; Score 12; DB 8; Length 8;
Pred. No. 1e+06;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XHV 7
DB 4 IXLKH 8

RESULT 12
Q15894 PRELIMINARY; PRT; 8 AA.
AC Q15894;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP587B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).

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DR EMBL; L32074; AAA73884.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 952 MW; EBC735B1E1F1B6D6 CRC64;

Query Match
Best Local Similarity 44.0%; Score 11; DB 4; Length 8;
Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XHV 7
DB 1 MOTH 5

RESULT 13
Q9UMC7 PRELIMINARY; PRT; 8 AA.
AC Q9UMC7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE SHMT protein (Fragment).
GN SHMT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Chave K.J., Snell K., Sanders P.G.;
RT "Isolation and characterization of human genomic sequences encoding
RT cytosolic serine hydroxymethyltransferase.";
RL Biochem. Soc. Trans. 25:53-53(1997).
DR EMBL; Y14492; CAB54844.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 868 MW; 7C205721E4AB5B8 CRC64;

Query Match
Best Local Similarity 44.0%; Score 11; DB 4; Length 8;
Pred. No. 1e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHV 8
DB 4 NHL 6

RESULT 14
Q9XSY1 PRELIMINARY; PRT; 8 AA.
AC Q9XSY1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Retinoblastoma protein (Fragment).
GN RBL.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97049323; PubMed=8894053;
RA Venta P.J., Brouillette J.A., Yuzbasilyan-Gurkan V., Brewer G.J.;
RT "Gene-specific universal mammalian sequence-tagged sites: application
RT to the canine genome.";
RL Biochem. Genet. 34:321-341(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Venta P.J., Cao Y., Alexander L., Yuzbasilyan-Gurkan V.;
RT "Dinucleotide repeat polymorphism in the canine retinoblastoma (RBL)
RT gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF155737; AAD38807.1; -  
 FT NON TER 1  
 SQ SEQUENCE 8 AA; 895 MW; 1425BBI8676721E3 CRC64;

Query Match 44.0%; Score 11; DB 6; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1e+06;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH1 8  
 DB 1 KHL 3

## RESULT 15

Q8MGC9 PRELIMINARY; PRT; 8 AA.  
 AC Q8MGC9;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE MADH dehydrogenase subunit 1 (Fragment).  
 OS Upogebia affinis.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Thalassinidea;  
 OC Callinassoidae; Upogebidae; Upogebia.  
 OK NCBI\_TaxID=177247;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,  
 RA Cunningham C.W.;  
 RT "Mitochondrial gene rearrangements support a hypothesis of parallel  
 evolution to the crab-like form."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF436047; AAL31621.1; -  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KM Mitochondrion.  
 FT NON TER 8  
 SQ SEQUENCE 8 AA; 978 MW; FE20573B5452C056 CRC64;

Query Match 44.0%; Score 11; DB 8; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 1e+06;  
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH1 8  
 DB 1 MIVVYL 6

RESULT 16  
 Q8L802 PRELIMINARY; PRT; 8 AA.  
 AC Q8L802;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Pat (Fragment).  
 GN PAT.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OK NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ranning S.B., Berdal K.G., Vaitilingom M.M., Holst-Jensen A.;  
 RT "Transformation event-specific quantitative real-time PCR for  
 RT genetically modified Btl maize (Zea mays) and estimation of the  
 RT impact of exogenous DNA on the limit of quantification."  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY123624; AAM89275.1; -  
 FT NON TER 1

SQ SEQUENCE 8 AA; 909 MW; 6046C1B2D77412D7 CRC64;

Query Match 44.0%; Score 11; DB 10; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1e+06;  
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH1 8  
 DB 3 RPTVQI 8

## RESULT 17

P79940 PRELIMINARY; PRT; 8 AA.  
 AC P79940;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Xmei1-4 protein (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OK NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97202105; PubMed=9049632;  
 RA Steelman S., Moskow J.J., Muzynski K., North C., Druck T.,  
 RA Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.;  
 RT "Identification of a conserved family of We1-1-related homeobox  
 RT genes."  
 RL Genome Res. 7:142-156(1997).  
 DR EMBL; U68389; AAB19199.1; -  
 DR TRANSFAC; T03410; -  
 FT NON TER 1  
 SQ SEQUENCE 8 AA; 1187 MW; 278B51F37B11F40B CRC64;

Query Match 44.0%; Score 11; DB 13; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 1e+06;  
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 QXXVXH 7  
 DB 1 ERBHM 6

RESULT 18  
 Q45615 PRELIMINARY; PRT; 8 AA.  
 AC Q45615;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE GUTB protein (Fragment).  
 GN GUTB.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OK NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=94253000; PubMed=8195086;  
 RA Ye R., Wong S.L.;  
 RT "Transcriptional regulation of the Bacillus subtilis glucitol  
 RT dehydrogenase gene."  
 RL J. Bacteriol. 176:3314-3320(1994).  
 DR EMBL; L16626; AAA20875.1; -  
 FT NON TER 8  
 SQ SEQUENCE 8 AA; 927 MW; FD56C772D1A1F1A6 CRC64;

Query Match 40.0%; Score 10; DB 2; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1e+06;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VXXH 7  
:::|  
Db 1 MTH 3

## RESULT 19

ID 09S443 PRELIMINARY; PRT; 8 AA.  
AC 09S443;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)  
DE Beta-lactamase (Fragment).  
GN PSE2.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R545;  
RA Roy D., Coulombe M., Perron K., Roy P.H.;  
RT "Characterization of a novel 6'-N-aminoglycoside acetyltransferase  
RT gene aac(6')-IIC from the integron of a Chinese Pseudomonas aeruginosa  
RT clinical isolate."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF162771; AAD46628.1; -.  
FT NON TER 8 8  
SQ SEQUENCE 8 AA; 930 MW; EBD5DDDD9D1A336 CRC64;

Query Match 40.0%; Score 10; DB 2; Length 8;  
Best Local Similarity 0.0%; Pred. No. 1e+06;  
Matches 0; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 XXXVXHI 8  
:::|  
Db 1 MKTFPAIV 8

## RESULT 20

ID 08G940 PRELIMINARY; PRT; 8 AA.  
AC 08G940;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, last annotation update)  
DE PF-50 protein (Fragment).  
GN PF-50.  
OS Borrelia burgdorferi ( Lyme disease spirochete).  
OC Plasmid group cp32-9, and Plasmid group cp32-12.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DN127C19-2, and Sh-2-82;  
RA PLASMID=group cp32-9, and group cp32-12;  
RA Stevenson B., Miller J.C.;  
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
RT prophages: conservation amidst diversity."  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY142104; AAN17853.1; -.  
DR EMBL; AY142097; AAN17907.1; -.  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
KM Plasmid.  
FT NON TER 1 1  
SQ SEQUENCE 8 AA; 1042 MW; 1437244330504373 CRC64;

Query Match 40.0%; Score 10; DB 2; Length 8;  
Best Local Similarity 0.0%; Pred. No. 1e+06;  
Matches 0; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXHI 8

Db 1 KWIINKL 7  
:::|  
Db 3 HNVVKI 8

## RESULT 21

ID 005403 PRELIMINARY; PRT; 8 AA.  
AC 005403;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)  
DE DNA for ORF. from chromosome XV (Fragment).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FY1679;  
RX MEDLINE=96021609; PubMed=8533473;  
RA Zumslein E., Pearson B.M., Kalogetopoulos A., Schweizer M.;  
RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains  
RT more than twice as many unknown as known open reading frames."  
RL Yeast 11:975-986(1995).  
DR EMBL; X83121; CAA58183.1; -.  
FT NON TER 8 8  
SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 40.0%; Score 10; DB 3; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1e+06;  
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXHI 8  
:::|  
Db 3 HNVVKI 8

## RESULT 22

ID 013591 PRELIMINARY; PRT; 8 AA.  
AC 013591;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)  
DE ORF YNL337W (Fragment).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Obermaler B., Piravandi E., Rinke M.;  
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA MIPS;  
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z71612; CAA96271.2; -.  
FT NON TER 1 1  
SQ SEQUENCE 8 AA; 1005 MW; 5CA441E449C9C720 CRC64;

Query Match 40.0%; Score 10; DB 3; Length 8;  
Best Local Similarity 20.0%; Pred. No. 1e+06;  
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXHI 7  
:::|  
Db 2 LFFNH 6

## RESULT 23

Q9BYT5 PRELIMINARY; PRT; 8 AA.

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AC Q9BY5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE cAMP responsive element moderator (Fragment).
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=11082082; PubMed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR GO: GO:0005634; C:nucleus; NAS.
DR GO: GO:0003677; F:DNA binding; NAS.
DR GO: GO:0006555; P:regulation of transcription, DNA-dependent; NAS.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1006 MW; DF02C331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 4; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06; 1; Indels 0; Gaps 0;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
DB 1 DLYCH 5

RESULT 24
Q9UDZ4 PRELIMINARY; PRT; 8 AA.
AC Q9UDZ4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RHD protein (Fragment).
GN RHD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97260406; PubMed=9106526;
RA Matsuoka G., Cherif-Zahar B., Mourou I., Carttron J.P.;
RT "Characterization of the recombination hot spot involved in the
RT genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
RT phenotype.";
RL Am. J. Hum. Genet. 60:808-817(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9306356; PubMed=1438298;
RA Le Van Kim C., Mourou I., Cherif-Zahar B., Raynal V., Cherrier C.,
RT "Molecular cloning and primary structure of the human blood group Rh
RT polypeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10925-10929(1992).
DR EMBL; Z97031; CAB09727.1; -.
DR GO: GO:0016021; C:integral to membrane; NAS.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1042 MW; D296944691FB5AB1 CRC64;

Query Match 40.0%; Score 10; DB 4; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06; 2; Mismatches 0; Indels 0;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 6 XHI 8
DB 3 YHM 5

RESULT 25
Q15893 PRELIMINARY; PRT; 8 AA.
AC Q15893;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP587A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90349591; PubMed=1696722;
RA Cherif-Zahar B., Bloy C., Le Van Kim C., Blanchard D., Bailly P.,
RT "Molecular cloning and protein structure of a human blood group Rh
RT polypeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6243-6247(1990).
DR EMBL; Z97030; CAB09726.1; -.

Query Match 40.0%; Score 10; DB 4; Length 8;
Best Local Similarity 16.7%; Pred. No. 1e+06; 5; Mismatches 0; Indels 0;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXVXH 6
DB 1 SQNPLQ 6

RESULT 26
Q9UMH9 PRELIMINARY; PRT; 8 AA.
AC Q9UMH9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RHCE protein (Fragment).
GN RHCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97260406; PubMed=9106526;
RA Matsuoka G., Cherif-Zahar B., Mourou I., Carttron J.P.;
RT "Characterization of the recombination hot spot involved in the
RT genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
RT phenotype.";
RL Am. J. Hum. Genet. 60:808-817(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90349591; PubMed=1696722;
RA Cherif-Zahar B., Bloy C., Le Van Kim C., Blanchard D., Bailly P.,
RT "Molecular cloning and protein structure of a human blood group Rh
RT polypeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6243-6247(1990).
DR EMBL; Z97030; CAB09726.1; -.

```

```
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1049 MW; C007244691FB5AB1 CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 4; Length 8;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHI 8
   :|:
Db 3 YHM 5

RESULT 27
Q81V87 PRELIMINARY; PRT; 8 AA.
ID Q81V87;
AC Q81V87;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-JUN-2003 (TREMBlrel. 23, last sequence update)
DE D1107712.2 (Serine palmitoyltransferase, long chain subunit
  2-like (Aminotransferase 2), variant 1) (Fragment).
GN SPTLC2L.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050320; CAD54807.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
KM Transferase.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 908 MW; 8E533682CEBB042 CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 4; Length 8;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXYXHI 8
   :|:|
Db 3 CCVMKI 8

RESULT 28
Q8MUN6 PRELIMINARY; PRT; 8 AA.
ID Q8MUN6;
AC Q8MUN6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN MPI.
OS Heliconius melpomene melpomene.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dityrsia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.
OX NCBI_TaxID=171917;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=STRI-B-441-Mpi-2;
RA Bull V., Beltman M., Bermingham E., Jiggins C., McMillan O.,
RA Mallet J.;
RL "Molecular evidence for gene flow between species of Heliconius.";
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516247; AAM61933.1; -.
DR GO; GO:0016853; F:isomerase activity; IEA.
KM Isomerase.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 977 MW; 16E736DB1D1EAA3 CRC64;
```

```
Query Match
Best Local Similarity 40.0%; Score 10; DB 5; Length 8;
Matches 1; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 X0XXVXH 7
   :|:|
Db 2 DHAEQLH 8

RESULT 29
Q86BS9 PRELIMINARY; PRT; 8 AA.
ID Q86BS9;
AC Q86BS9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, last sequence update)
DE Cyclin B (Fragment).
GN CYCLIN B.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96027756; PubMed=7546293;
RA Thatcher J.D., McBride B., Katula K.S.;
RT "Promoter binding factors regulating cyclin B transcription in the sea
  urchin embryo.";
RL DNA Cell Biol. 14:869-881 (1995).
DR EMBL; S80441; AAP32224.1; -.
KM Cyclin.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 897 MW; EE645411ADD1EDD6 CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 5; Length 8;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VXH 7
   :|
Db 1 MAH 3

RESULT 30
Q9TT78 PRELIMINARY; PRT; 8 AA.
ID Q9TT78;
AC Q9TT78;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Thymidylate synthase (Fragment).
GN TS.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015404; PubMed=11130975;
RA Brouillette J.A., Andrew J.R., Venta P.J.;
RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
  method.";
RL Mamm. Genome 11:1079-1086 (2000).
DR EMBL; AF202073; AAF20918.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 899 MW; 6731A1B059CA867 CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 6; Length 8;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

OY 3 XXVXH 7  
Db 2 DLYCH 6

## RESULT 31

O9BF82 PRELIMINARY; PRT; 8 AA.  
AC O9BF82; (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
GN CAMP responsive element moderator (Fragment).  
OS Ursus arctos (Brown bear) (Grizzly bear).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.  
OX NCBI\_TaxID=9644;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21082082; PubMed=11214319;  
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
RT "Molecular phylogenetics and the origins of placental mammals."  
RL Nature 409:614-618(2001).  
DR EMBL: AY011663; AAC47591.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;  
Best Local Similarity 20.0%; Pred. No. 1e+06;  
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7  
Db 1 DLYCH 5

## RESULT 32

O9BFC2 PRELIMINARY; PRT; 8 AA.  
AC O9BFC2; (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
GN CAMP responsive element moderator (Fragment).  
OS Macropus eugenii (Tamar wallaby).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.  
OX NCBI\_TaxID=9315;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21082082; PubMed=11214319;  
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
RT "Molecular phylogenetics and the origins of placental mammals."  
RL Nature 409:614-618(2001).  
DR EMBL: AY011621; AAC47536.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;  
Best Local Similarity 20.0%; Pred. No. 1e+06;  
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7  
Db 1 DLYCH 5

## RESULT 33

O9BF90 PRELIMINARY; PRT; 8 AA.  
AC O9BF90; (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
GN CAMP responsive element moderator (Fragment).  
OS Tragelaphus eurycerus (Bongo).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Tragelaphus.  
OX NCBI\_TaxID=69297;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21082082; PubMed=11214319;  
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
RT "Molecular phylogenetics and the origins of placental mammals."  
RL Nature 409:614-618(2001).  
DR EMBL: AY011673; AAC47583.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;  
Best Local Similarity 20.0%; Pred. No. 1e+06;  
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7  
Db 1 DLYCH 5

## RESULT 34

O9BFB1 PRELIMINARY; PRT; 8 AA.  
AC O9BFB1; (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
GN CAMP responsive element moderator (Fragment).  
OS Echinops telfairi (Lesser hedgehog tenrec).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Echinops.  
OX NCBI\_TaxID=9371;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21082082; PubMed=11214319;  
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
RT "Molecular phylogenetics and the origins of placental mammals."  
RL Nature 409:614-618(2001).  
DR EMBL: AY011632; AAC47547.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;  
Best Local Similarity 20.0%; Pred. No. 1e+06;  
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7  
Db 1 DLYCH 5

## RESULT 35

O9BFA1 PRELIMINARY; PRT; 8 AA.  
AC O9BFA1; (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

```

DE  CAMP responsive element moderator (Fragment).
GN  CREM.
OS  Ateles fusciceps (Brown-headed spider monkey).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.
OX  NCBI_TaxID=9508;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21082082; PubMed=11214319;
RA  Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA  O'Brien S.J.;
RT  "Molecular phylogenetics and the origins of placental mammals.";
RL  Nature 409:614-618(2001).
DR  EMBL; AY011660; AAG47571.1; -.
FT  NON TER
SQ  SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match      40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY  3 XXVXH 7
    :: :|
Db  1 DLYCH 5

RESULT 36
Q9BFB7  PRELIMINARY; PRT; 8 AA.
AC  Q9BFB7;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE  CAMP responsive element moderator (Fragment).
GN  CREM.
OS  Tapirus indicus (Asiatic tapir) (Malayan capri).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX  NCBI_TaxID=9802;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21082082; PubMed=11214319;
RA  Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA  O'Brien S.J.;
RT  "Molecular phylogenetics and the origins of placental mammals.";
RL  Nature 409:614-618(2001).
DR  EMBL; AY011678; AAG47586.1; -.
FT  NON TER
SQ  SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match      40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY  3 XXVXH 7
    :: :|
Db  1 DLYCH 5

RESULT 37
Q9BFB9  PRELIMINARY; PRT; 8 AA.
AC  Q9BFB9;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-DIC-2001 (TrEMBLrel. 19, Last annotation update)
DE  CAMP responsive element moderator (Fragment).
GN  CREM.
OS  Euphractus sexcinctus (Six-banded armadillo).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Edentata; Dasypodidae; Euphractus.
OX  NCBI_TaxID=143300;
RN  [1]

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RP  SEQUENCE FROM N.A.
RX  MEDLINE=21082082; PubMed=11214319;
RA  Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA  O'Brien S.J.;
RT  "Molecular phylogenetics and the origins of placental mammals.";
RL  Nature 409:614-618(2001).
DR  EMBL; AY011624; AAG47539.1; -.
FT  NON TER
SQ  SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match      40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY  3 XXVXH 7
    :: :|
Db  1 DLYCH 5

RESULT 38
Q9BFB8  PRELIMINARY; PRT; 8 AA.
AC  Q9BFB8;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE  CAMP responsive element moderator (Fragment).
GN  CREM.
OS  Chaetophractus villosus (South American armadillo).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Edentata; Dasypodidae; Chaetophractus.
OX  NCBI_TaxID=29080;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21082082; PubMed=11214319;
RA  Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA  O'Brien S.J.;
RT  "Molecular phylogenetics and the origins of placental mammals.";
RL  Nature 409:614-618(2001).
DR  EMBL; AY011625; AAG47540.1; -.
FT  NON TER
SQ  SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match      40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY  3 XXVXH 7
    :: :|
Db  1 DLYCH 5

RESULT 39
Q9BFA0  PRELIMINARY; PRT; 8 AA.
AC  Q9BFA0;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  CAMP responsive element moderator (Fragment).
GN  CREM.
OS  Macaca mulatta (Rhesus macaque).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC  Cercopithecinae; Macaca.
OX  NCBI_TaxID=9544;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=21082082; PubMed=11214319;
RA  Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA  O'Brien S.J.;
RT  "Molecular phylogenetics and the origins of placental mammals.";
RL  Nature 409:614-618(2001).

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DR EMBL; AY011661; AAC47572.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 1006 MW; DF02C31EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7
   :: :|
Db 1 DLVCH 5

RESULT 40
O9BFA8 PRELIMINARY; PRT; 8 AA.
AC O9BFA8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Loxodonta africana (African elephant).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Loxodonta.
OX NCBI_TaxID=9785;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011635; AAC47550.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7
   :: :|
Db 1 DLVCH 5

RESULT 41
O9BFA9 PRELIMINARY; PRT; 8 AA.
AC O9BFA9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Procavia capensis (Cape hyrax) (Rock dassie).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Hyracoidea; Procaviidae; Procavia.
OX NCBI_TaxID=9813;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011634; AAC47549.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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OY 3 XXVXH 7
   :: :|
Db 1 DLVCH 5

RESULT 42
O9BFB2 PRELIMINARY; PRT; 8 AA.
AC O9BFB2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Sorex araneus (Eurasian common shrew) (European shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex.
OX NCBI_TaxID=42254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011631; AAC47546.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7
   :: :|
Db 1 DLVCH 5

RESULT 43
O9BFB5 PRELIMINARY; PRT; 8 AA.
AC O9BFB5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Erinaceus concolor (Eastern European hedgehog) (Erinaceus roumanicus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=37316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011628; AAC47543.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 XXVXH 7
   :: :|
Db 1 DLVCH 5

RESULT 44

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Q9BFB6
ID Q9BFB6 PRELIMINARY; PRT; 8 AA.
AC Q9BFB6;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Myrmecophaga tridactyla (Giant anteater).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Myrmecophagidae; Myrmecophaga.
OX NCBI_TaxID=71006;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011627; AAG47542.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

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Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 3 XXVXH 7
DB 1 DLYCH 5

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ID Q9BFB3;
AC Q9BFB3;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Condylura cristata (Star-nosed mole).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Talpidae; Condylura.
OX NCBI_TaxID=143302;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011630; AAG47545.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

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Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 3 XXVXH 7
DB 1 DLYCH 5

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Search completed: August 19, 2004, 15:50:49  
 Job time : 31 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2004, 15:47:57 ; Search time 13.5 Seconds  
(without alignments)  
30.593 Million cell updates/sec

Title: VARIANT1  
Perfect score: 25  
Sequence: 1 XQXVXVHL 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 13858

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	8	1 US-08-168-390-11	Sequence 11, Appl
2	25	100.0	8	1 US-08-168-390-12	Sequence 12, Appl
3	25	100.0	8	2 US-08-337-127-9	Sequence 9, Appl
4	25	100.0	8	4 US-09-260-846-9	Sequence 9, Appl
5	25	100.0	8	4 US-09-248-381-16	Sequence 16, Appl
6	25	100.0	8	4 US-09-248-381-17	Sequence 17, Appl
7	25	100.0	8	6 5217955-32	Patent No. 5217955
8	25	100.0	8	6 5217955-34	Patent No. 5217955
9	25	100.0	8	6 5217955-35	Patent No. 5217955
10	25	100.0	8	6 5217955-36	Patent No. 5217955
11	23	92.0	8	4 US-09-248-381-18	Sequence 18, Appl
12	23	92.0	8	4 US-09-248-381-19	Sequence 19, Appl
13	23	88.0	8	6 5217955-37	Patent No. 5217955
14	21	84.0	8	1 US-08-031-325A-27	Sequence 27, Appl
15	21	84.0	8	2 US-08-337-127-4	Sequence 4, Appl
16	21	84.0	8	2 US-08-337-127-8	Sequence 8, Appl
17	21	84.0	8	4 US-09-260-846-4	Sequence 4, Appl
18	21	84.0	8	4 US-09-260-846-8	Sequence 8, Appl
19	21	84.0	8	4 US-09-248-381-6	Sequence 6, Appl
20	21	84.0	8	6 5217955-31	Patent No. 5217955
21	21	84.0	8	6 5217955-33	Patent No. 5217955
22	21	84.0	8	6 5217955-38	Patent No. 5217955
23	20	80.0	8	1 US-08-168-390-13	Sequence 13, Appl
24	20	80.0	8	1 US-08-168-390-14	Sequence 14, Appl
25	19	76.0	8	1 US-08-387-634-3	Sequence 3, Appl
26	19	76.0	8	4 US-09-515-965A-1846	Sequence 1846, Ap
27	19	76.0	8	6 5217955-25	Patent No. 5217955

28	19	76.0	8	6 5217955-27	Patent No. 5217955
29	19	76.0	8	6 5217955-28	Patent No. 5217955
30	18	72.0	8	3 US-08-444-818-632	Sequence 632, App
31	18	72.0	8	3 US-09-011-961-16	Sequence 16, Appl
32	18	72.0	8	4 US-09-428-082B-537	Sequence 537, App
33	18	72.0	8	4 US-09-428-082B-539	Sequence 539, App
34	17	68.0	8	1 US-08-427-993B-4	Sequence 4, Appl
35	17	68.0	8	2 US-08-478-609A-4	Sequence 4, Appl
36	17	68.0	8	3 US-08-416-346-20	Sequence 20, Appl
37	17	68.0	8	3 US-08-444-818-375	Sequence 375, App
38	17	68.0	8	3 US-08-444-818-633	Sequence 633, App
39	17	68.0	8	3 US-09-335-411-20	Sequence 20, Appl
40	17	68.0	8	4 US-09-515-965A-1889	Sequence 1889, Ap
41	16	64.0	8	1 US-07-872-644-34	Sequence 34, Appl
42	16	64.0	8	1 US-08-297-494-34	Sequence 34, Appl
43	16	64.0	8	1 US-08-297-510-34	Sequence 34, Appl
44	16	64.0	8	1 US-08-479-532-34	Sequence 34, Appl
45	16	64.0	8	1 US-08-571-985-22	Sequence 22, Appl

#### ALIGNMENTS

RESULT 1  
US-08-168-390-11  
; Sequence 11, Application US/08168390  
; Patent No. 5620955  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazuyuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELETYPE: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note="The amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical end caps."  
; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: /note="The carboxy-terminal  
; OTHER INFORMATION: residue comprises an ethyl ester."  
; US-08-168-390-11

Query Match 100.0%; Score 25; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3e+05;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 XXXVXHL 8  
Db 1 NQNAVGH 8

RESULT 2  
US-08-168-390-12  
; Sequence 12, Application US/08168390  
; Patent No. 562055  
; GENERAL INFORMATION:  
; APPLICANT: Knight, Martha  
; APPLICANT: Takahashi, Kazuyuki  
; APPLICANT: Chandrasekhar, Bhaskar  
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/168,390  
; FILING DATE: Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldstein, Jorge A.  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0871.0040001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; TELEX: 248636 SKK  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "The amino-terminal residue  
; OTHER INFORMATION: comprises one of several chemical end caps."  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 6  
; OTHER INFORMATION: /note= "The alanine at position 6  
; OTHER INFORMATION: is dextrorotatory alanine."  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 8  
; OTHER INFORMATION: /note= "The carboxy-terminal  
; OTHER INFORMATION: residue comprises an ethyl ester."  
; US-08-168-390-12

Query Match 100.0%; Score 25; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3e+05;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 XXXVXHL 8  
Db 1 NQNAVGH 8

RESULT 3  
US-08-337-127-9  
; Sequence 9, Application US/08337127  
; Patent No. 5877277  
; GENERAL INFORMATION:  
; APPLICANT: Coy, David H.  
; APPLICANT: Moreau, Jacques-Pierre  
; APPLICANT: Kim, Sun H.  
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN  
; TITLE OF INVENTION: ANALOGS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
; COMPUTER: IBM PS/2 Model 50z or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: Wordperfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/337,127  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/779,039  
; FILING DATE: 10/18/91  
; APPLICATION NUMBER: 07/502,438  
; FILING DATE: 03/30/90  
; APPLICATION NUMBER: 07/397,169  
; FILING DATE: 08/21/89  
; APPLICATION NUMBER: 07/376,555  
; FILING DATE: 07/07/89  
; APPLICATION NUMBER: 07/317,941  
; FILING DATE: 03/02/89  
; APPLICATION NUMBER: 07/282,328  
; FILING DATE: 12/09/88  
; APPLICATION NUMBER: 07/257,998  
; FILING DATE: 10/14/88  
; APPLICATION NUMBER: 07/248,771  
; FILING DATE: 09/23/88  
; APPLICATION NUMBER: 07/207,759  
; FILING DATE: 06/16/88  
; APPLICATION NUMBER: 07/204,171  
; FILING DATE: 06/08/88  
; APPLICATION NUMBER: 07/173,311  
; FILING DATE: 03/25/88  
; APPLICATION NUMBER: 07/100,571  
; FILING DATE: 09/24/87  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00537/00900D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: The sequence contains at  
; OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,  
; OTHER INFORMATION: and has an methyllester C-terminus (i.e., COOCH3),  
; OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., COOH).

US-09-337-127-9

Query Match 100.0%; Score 25; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 4; Mismatches 0;

QY 1 XQXXVXHL 8  
1 EOWAVGHL 8

RESULT 4  
US-09-260-846-9  
Sequence 9, Application US/09260846  
Patent No. 6307017  
GENERAL INFORMATION:  
APPLICANT: COY, David H.  
APPLICANT: Moreau, Jacques-Pierre  
APPLICANT: Kim, Sun Hyuk  
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS  
FILE REFERENCE: 00537/0090001  
CURRENT APPLICATION NUMBER: US/09/260,846  
CURRENT FILING DATE: 1999-03-02  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 9  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: pyroglutamate  
FEATURE:  
OTHER INFORMATION: this peptide has a methyllester c-terminus  
US-09-260-846-9

Query Match 100.0%; Score 25; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 4; Mismatches 0;

QY 1 XQXXVXHL 8  
1 EOWAVGHL 8

RESULT 5  
US-09-248-381-16  
Sequence 16, Application US/09248381  
Patent No. 6492330  
GENERAL INFORMATION:  
APPLICANT: MUKHERJEE, RAMA  
APPLICANT: JAGGI, MANU  
APPLICANT: PRASAD, SUDHANAND  
APPLICANT: BURMAN, ANAND C  
APPLICANT: RAJENDRAN, PRAVEEN  
APPLICANT: NATHUR, ARCHANA  
APPLICANT: SINGH, ANU T  
TITLE OF INVENTION: ANTITUMORIC DRUGS  
FILE REFERENCE: U 011695-8  
CURRENT APPLICATION NUMBER: US/09/248,381  
CURRENT FILING DATE: 1999-02-11  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 16  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: This peptide  
OTHER INFORMATION: was synthetically generated.

FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe;  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (4)  
OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Alb  
US-09-248-381-16

Query Match 100.0%; Score 25; DB 4; Length 8;  
Best Local Similarity 75.0%; Pred. No. 3e+05; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 0;

QY 1 XQXXVXHL 8  
1 XQWVXGHL 8

RESULT 6  
US-09-248-381-17  
Sequence 17, Application US/09248381  
Patent No. 6492330  
GENERAL INFORMATION:  
APPLICANT: MUKHERJEE, RAMA  
APPLICANT: JAGGI, MANU  
APPLICANT: PRASAD, SUDHANAND  
APPLICANT: BURMAN, ANAND C  
APPLICANT: RAJENDRAN, PRAVEEN  
APPLICANT: NATHUR, ARCHANA  
APPLICANT: SINGH, ANU T  
TITLE OF INVENTION: ANTITUMORIC DRUGS  
FILE REFERENCE: U 011695-8  
CURRENT APPLICATION NUMBER: US/09/248,381  
CURRENT FILING DATE: 1999-02-11  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 17  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: This peptide  
OTHER INFORMATION: was synthetically generated.  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (6)  
OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Alb  
US-09-248-381-17

Query Match 100.0%; Score 25; DB 4; Length 8;  
Best Local Similarity 75.0%; Pred. No. 3e+05; Indels 0; Gaps 0;  
Matches 6; Conservative 2; Mismatches 0;

QY 1 XQXXVXHL 8  
1 XQWVXGHL 8

RESULT 7  
5217955-32  
Patent No. 5217955  
APPLICANT: ABOGDE, ARTHUR E.; MOREAU, JACQUES-PIERRE  
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
NUMBER OF SEQUENCES: 42  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,225  
FILING DATE: 09-MAY-1990

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:32:
; LENGTH: 8
5217955-32
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Query Match          100.0%; Score 25; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Db      1 FQWAVGHL 8
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RESULT 8
5217955-34
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:34:
; LENGTH: 8
5217955-34
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Query Match          100.0%; Score 25; DB 6; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Db      1 XQWAVGHL 8
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RESULT 9
5217955-35
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:35:
; LENGTH: 8
5217955-35
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```
Query Match          100.0%; Score 25; DB 6; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Db      1 XQWAVGHL 8
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RESULT 10
5217955-36
; Patent No. 5217955
; APPLICANT: ABOGDEN, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:36:
; LENGTH: 8
5217955-36
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Query Match          100.0%; Score 25; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Db      1 FQWAVGHL 8
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RESULT 11
US-09-248-381-18
; Sequence 18, Application US/09248381
; Patent No. 6492330
; GENERAL INFORMATION:
; APPLICANT: MUKHERJEE, RAMA
; APPLICANT: JAGGI, MANU
; APPLICANT: PRASAD, SUDHANAND
; APPLICANT: BURMAN, ANAND C
; APPLICANT: RAJENDRAN, PRAVEEN
; APPLICANT: MATUR, ARCHANA
; APPLICANT: SINGH, ANU T
; TITLE OF INVENTION: ANTIANGIOGENIC DRUGS
; FILE REFERENCE: U 011695-8
; CURRENT APPLICATION NUMBER: US/09/248,381
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This peptide
; OTHER INFORMATION: was synthetically generated.
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)_RES
; OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Aib
; US-09-248-381-18
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Query Match          92.0%; Score 23; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Db      1 XQWVGH1 8
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RESULT 12  
US-09-248-381-19  
; Sequence 19, Application US/09248381  
; Patent No. 6492330  
; GENERAL INFORMATION:  
; APPLICANT: MUKHERJEE, RAMA  
; APPLICANT: JAGGI, MANU  
; APPLICANT: PRASAD, SUDHANAND  
; APPLICANT: BURMAN, ANAND C  
; APPLICANT: RAJENDRAN, PRAVEEN  
; APPLICANT: MATHUR, ARCHANA  
; APPLICANT: SINGH, ANU T  
; TITLE OF INVENTION: ANTIANGIOGENIC DRUGS  
; FILE REFERENCE: U 011695-8  
; CURRENT APPLICATION NUMBER: US/09/248,381  
; CURRENT FILING DATE: 1999-02-11  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: This peptide  
; OTHER INFORMATION: was synthetically generated.  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (6)  
; OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Alb  
US-09-248-381-19

Query Match 92.0%; Score 23; DB 4; Length 8;  
Best Local Similarity 62.5%; Pred. No. 3e+05;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHL 8  
DB 1 XQWAVXHI 8

RESULT 13  
5217955-37  
; Patent No. 5217955  
; APPLICANT: ABOGDE, ARTHUR E.; MOREAU, JACQUES-PIERRE  
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/520,225  
; FILING DATE: 09-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 440-039  
; FILING DATE: 21-NOV-1989  
; APPLICATION NUMBER: 408,125  
; FILING DATE: 15-SEP-1989  
; SEQ ID NO:37:  
; LENGTH: 8  
5217955-37

Query Match 88.0%; Score 22; DB 6; Length 8;  
Best Local Similarity 37.5%; Pred. No. 3e+05;  
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHL 8  
DB 1 FEWAVXHL 8

RESULT 14

US-08-031-325A-27  
; Sequence 27, Application US/08031325A  
; Patent No. 5369094  
; GENERAL INFORMATION:  
; APPLICANT: Schally, Andrew V.  
; APPLICANT: Cai, Renzhi  
; TITLE OF INVENTION: POLYPEPTIDE BOMBESIN ANTAGONISTS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OMRI M. BEHR, ESO  
; STREET: 325 PIERSON AVENUE  
; CITY: EDISON  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 08837  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/031,325A  
; FILING DATE: 15-MAR-1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/619,747  
; FILING DATE: 29-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BEHR, OMRI M.  
; REGISTRATION NUMBER: 22,940  
; REFERENCE/DOCKET NUMBER: SHAL3.0-014  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 494-5240  
; TELEFAX: (908) 494-0428  
; TELEX: 511642 BEPATEDIN  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1  
; OTHER INFORMATION: /note= "Res 1 = (R1) (R2)-A0-Al, where A0  
; OTHER INFORMATION: = deleted; Al = D-Phe, D-Tip or D-Nal; R1 and R2 = H"  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 8  
; OTHER INFORMATION: /note= "Res 8 = A8-W, where W = -N(R8)-  
; OTHER INFORMATION: CH(Z1)-R4-CH(Z2)-CO-V, where R4 = CH2NH; Z1 = -CH2CH(CH3)2; Z2  
; OTHER INFORMATION: H or  
; OTHER INFORMATION: COB1, where E1 = Cl-20 alkyl"  
US-08-031-325A-27

Query Match 84.0%; Score 21; DB 1; Length 8;  
Best Local Similarity 57.1%; Pred. No. 3e+05;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHL 7  
DB 1 XQWAVXGH 7

RESULT 15  
US-08-337-127-4  
; Sequence 4, Application US/08337127  
; Patent No. 5877277  
; GENERAL INFORMATION:  
; APPLICANT: Coy, David H.  
; APPLICANT: Moreau, Jacques-Pierre

APPLICANT: Kim, Sun H.  
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN  
TITLE OF INVENTION: ANALOGS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
SOFTWARE: WordPerfect (Version 5.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/337,127  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/779,039  
FILING DATE: 10/18/91  
APPLICATION NUMBER: 07/502,438  
FILING DATE: 03/30/90  
APPLICATION NUMBER: 07/397,169  
FILING DATE: 08/21/89  
APPLICATION NUMBER: 07/376,555  
FILING DATE: 07/07/89  
APPLICATION NUMBER: 07/317,941  
FILING DATE: 03/02/89  
APPLICATION NUMBER: 07/282,328  
FILING DATE: 12/09/88  
APPLICATION NUMBER: 07/257,998  
FILING DATE: 10/14/88  
APPLICATION NUMBER: 07/248,771  
FILING DATE: 09/23/88  
APPLICATION NUMBER: 07/207,759  
FILING DATE: 06/16/88  
APPLICATION NUMBER: 07/204,171  
FILING DATE: 06/08/88  
APPLICATION NUMBER: 07/173,311  
FILING DATE: 03/25/88  
APPLICATION NUMBER: 07/100,571  
FILING DATE: 09/24/87  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00537/00900D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: The sequence contains at  
OTHER INFORMATION: position 1 a pyroglutamate,  
OTHER INFORMATION: and has an amide C-terminus (i.e., COYNH2), rather  
OTHER INFORMATION: than  
OTHER INFORMATION: a carboxyl C-terminus (i.e., COYOH). Xaa stands for  
OTHER INFORMATION: statine.  
US-08-337-127-4

Query Match 84.0%; Score 21; DB 2; Length 8;  
Best Local Similarity 42.9%; Pred. No. 3e+05;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 XQXXVXH 7

Db :|:|:|  
1 EQWAVGH 7  
RESULT 16  
US-08-337-127-8  
Sequence 8, Application US/08337127  
Patent No. 5877277  
GENERAL INFORMATION:  
APPLICANT: Coy, David H.  
APPLICANT: Moreau, Jacques-Pierre  
APPLICANT: Kim, Sun H.  
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN  
TITLE OF INVENTION: ANALOGS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
SOFTWARE: WordPerfect (Version 5.0)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/337,127  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/779,039  
FILING DATE: 10/18/91  
APPLICATION NUMBER: 07/502,438  
FILING DATE: 03/30/90  
APPLICATION NUMBER: 07/397,169  
FILING DATE: 08/21/89  
APPLICATION NUMBER: 07/376,555  
FILING DATE: 07/07/89  
APPLICATION NUMBER: 07/317,941  
FILING DATE: 03/02/89  
APPLICATION NUMBER: 07/282,328  
FILING DATE: 12/09/88  
APPLICATION NUMBER: 07/257,998  
FILING DATE: 10/14/88  
APPLICATION NUMBER: 07/248,771  
FILING DATE: 09/23/88  
APPLICATION NUMBER: 07/207,759  
FILING DATE: 06/16/88  
APPLICATION NUMBER: 07/204,171  
FILING DATE: 06/08/88  
APPLICATION NUMBER: 07/173,311  
FILING DATE: 03/25/88  
APPLICATION NUMBER: 07/100,571  
FILING DATE: 09/24/87  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00537/00900D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: The sequence contains at  
OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,  
OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,

OTHER INFORMATION: and has an methyl ester C-terminus (i.e., COYCH3),  
OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., COYOH).  
US-08-337-127-8

Query Match 84.0%; Score 21; DB 2; Length 8;  
Best Local Similarity 42.9%; Pred. No. 3e+05;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7  
DB 1 EQWAVGH 7

RESULT 17  
US-09-260-846-4  
Sequence 4, Application US/09260846  
Patent No. 6307017  
GENERAL INFORMATION:  
APPLICANT: Coy, David H.  
APPLICANT: Moreau, Jacques-Pierre  
APPLICANT: Kim, Sun Hyuk  
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS  
FILE REFERENCE: 00537/009000  
CURRENT APPLICATION NUMBER: US/09/260,846  
CURRENT FILING DATE: 1999-03-02  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 4  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide

NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: pyroglutamate  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (8)  
OTHER INFORMATION: statine  
FEATURE:  
OTHER INFORMATION: this peptide has an amidated c-terminus  
US-09-260-846-4

Query Match 84.0%; Score 21; DB 4; Length 8;  
Best Local Similarity 42.9%; Pred. No. 3e+05;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7  
DB 1 EQWAVGH 7

RESULT 18  
US-09-260-846-8  
Sequence 8, Application US/09260846  
Patent No. 6307017  
GENERAL INFORMATION:  
APPLICANT: Coy, David H.  
APPLICANT: Moreau, Jacques-Pierre  
APPLICANT: Kim, Sun Hyuk  
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS  
FILE REFERENCE: 00537/009000  
CURRENT APPLICATION NUMBER: US/09/260,846  
CURRENT FILING DATE: 1999-03-02  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

US-09-260-846-8  
Sequence 8, Application US/09260846  
Patent No. 6307017  
GENERAL INFORMATION:  
APPLICANT: Coy, David H.  
APPLICANT: Moreau, Jacques-Pierre  
APPLICANT: Kim, Sun Hyuk  
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS  
FILE REFERENCE: 00537/009000  
CURRENT APPLICATION NUMBER: US/09/260,846  
CURRENT FILING DATE: 1999-03-02  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 8  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: pyroglutamate  
FEATURE:  
OTHER INFORMATION: this peptide has a methyl ester c-terminus  
US-09-260-846-8

Query Match 84.0%; Score 21; DB 4; Length 8;  
Best Local Similarity 42.9%; Pred. No. 3e+05;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7  
DB 1 EQWAVGH 7

RESULT 19  
US-09-248-381-6  
Sequence 6, Application US/09248381  
Patent No. 6492330  
GENERAL INFORMATION:  
APPLICANT: MURHERJEE, RAMA  
APPLICANT: JAGGI, MANU  
APPLICANT: PRASAD, SUDHANAND  
APPLICANT: BURMAN, ANAND C  
APPLICANT: RAJENDRAN, PRAVEEN  
APPLICANT: MAHUR, ARCHANA  
APPLICANT: SINGH, ANU T  
TITLE OF INVENTION: ANTITUMORIC DRUGS  
FILE REFERENCE: U 011695-8  
CURRENT APPLICATION NUMBER: US/09/248,381  
CURRENT FILING DATE: 1999-02-11  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 6  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: This peptide  
OTHER INFORMATION: was synthetically generated.  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (8)  
OTHER INFORMATION: /product=leucine N-ethylamide/label=Leu-NHET  
US-09-248-381-6

Query Match 84.0%; Score 21; DB 4; Length 8;  
Best Local Similarity 57.1%; Pred. No. 3e+05;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7  
DB 1 XQWAVGH 7

RESULT 20  
5217955-31  
Patent No. 5217955  
APPLICANT: ABOODEN, ARTHUR B.; MOREAU, JACQUES-PIERRE  
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
OF BOMBESIN, GRP, LITORIN OR NEUBROMEDIN  
NUMBER OF SEQUENCES: 42  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,225  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 440,039  
FILING DATE: 21-NOV-1989  
APPLICATION NUMBER: 408,125  
FILING DATE: 15-SEP-1989  
SEQ ID NO:31:  
LENGTH: 8  
5217955-31

Query Match 84.0%; Score 21; DB 6; Length 8;  
Best Local Similarity 57.1%; Pred. No. 3e+05;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7  
:|:|:|  
DB 1 XQWAVGH 7

RESULT 21  
5217955-33  
Patent No. 5217955  
APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
NUMBER OF SEQUENCES: 42  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,225  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 440,039  
FILING DATE: 21-NOV-1989  
APPLICATION NUMBER: 408,125  
FILING DATE: 15-SEP-1989  
SEQ ID NO:33:  
LENGTH: 8  
5217955-33

Query Match 84.0%; Score 21; DB 6; Length 8;  
Best Local Similarity 42.9%; Pred. No. 3e+05;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7  
:|:|:|  
DB 1 EQWAVGH 7

RESULT 22  
5217955-38  
Patent No. 5217955  
APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
NUMBER OF SEQUENCES: 42  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,225  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 440,039  
FILING DATE: 21-NOV-1989  
APPLICATION NUMBER: 408,125  
FILING DATE: 15-SEP-1989  
SEQ ID NO:38:  
LENGTH: 8  
5217955-38

Query Match 84.0%; Score 21; DB 6; Length 9;  
Best Local Similarity 42.9%; Pred. No. 3e+05;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7  
:|:|:|  
DB 1 EQWAVGH 7

RESULT 23  
US-08-168-390-13  
Sequence 13, Application US/08168390  
Patent No. 5620955  
GENERAL INFORMATION:  
APPLICANT: Knight, Martha  
APPLICANT: Takahashi, Kazayuki  
TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/168,390  
FILING DATE: Herewith

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0871.0040001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
TELEX: 248636 SSK

INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: Modified-site

LOCATION: 1  
OTHER INFORMATION: /note= "The amino-terminal residue  
comprises one of several chemical end caps."

FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: /note= "The carboxy-terminal  
residue comprises an ethyl ester."  
US-08-168-390-13

Query Match 80.0%; Score 20; DB 1; Length 8;  
Best Local Similarity 37.5%; Pred. No. 3e+05;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXH 8  
:|:|:|  
DB 1 NHWAVGHL 8

RESULT 24  
US-08-168-390-14  
Sequence 14, Application US/08168390  
Patent No. 5620955  
GENERAL INFORMATION:

APPLICANT: Knight, Martha  
APPLICANT: Takahashi, Kazayuki  
APPLICANT: Chandrasekhar, Bhaskar

TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600



CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/168,390  
FILING DATE: Herewith  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0871.0040001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
TELEX: 248636 SSK  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note= "The amino-terminal residue  
OTHER INFORMATION: comprises one of several chemical end caps."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6  
OTHER INFORMATION: /note= "The alanine at position 6  
OTHER INFORMATION: is dextrorotatory alanine."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: /note= "The carboxy-terminal  
OTHER INFORMATION: residue comprises an ethyl ester."  
US-08-168-390-14  
Query Match 80.0%; Score 20; DB 1; Length 8;  
Best Local Similarity 37.5%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;  
Matches 3; Conservative 4; Mismatches 1;  
QY 1 XXXVXHL 8  
DB 1 NHVAVHL 8  
RESULT 25  
US-08-387-634-3  
Sequence 3, Application US/08387634  
Patent No. 5767235  
GENERAL INFORMATION:  
APPLICANT: Kim, Sun Hyuk  
APPLICANT: Moreau, Jacques-Pierre  
TITLE OF INVENTION: LINEAR THERAPEUTIC PEPTIDES  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,634  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/929,306A  
FILING DATE: 08/13/92  
APPLICATION NUMBER: US/07/520,226  
FILING DATE: 05/09/90  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T. and Tsao, Y. Rocky  
REGISTRATION NUMBER: 30,162 and 34,053  
REFERENCE/DOCKET NUMBER: 00537/040002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8  
TYPE: amino acid  
STRANDEDNESS: N/A  
TOPOLOGY: N/A  
FEATURE:  
OTHER INFORMATION:  
OTHER INFORMATION: The sequence contains at position 1 an acetylated His, rather  
OTHER INFORMATION: than a His, and has an amide C-terminus (i.e., COOH).  
US-08-387-634-3  
Query Match 76.0%; Score 19; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3e+05;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 3 XXVXHL 8  
DB 2 WVGXHL 7  
RESULT 26  
US-09-515-965A-1846  
Sequence 1846, Application US/09515965A  
Patent No. 6623741  
GENERAL INFORMATION:  
APPLICANT: Antczak, J.  
APPLICANT: Delmedico, M.  
APPLICANT: Erickson, J.  
APPLICANT: Lambert, D.  
APPLICANT: Sista, P.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-  
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION  
FILE REFERENCE: 7872-073  
CURRENT APPLICATION NUMBER: US/09/515,965A  
CURRENT FILING DATE: 2000-02-29  
PRIOR APPLICATION NUMBER: 09/315,304  
PRIOR FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1994  
SOFTWARE: FastSeq for windows Version 3.0  
SEQ ID NO 1846  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-515-965A-1846  
Query Match 76.0%; Score 19; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3e+05;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 3 XXVXHL 8  
DB 4 WVGXHL 8

Db 3 SKVXHL 8

RESULT 27

5217955-25

Patent No. 5217955

APPLICANT: ABOGDEEN, ARTHUR E.; MOREAU, JACQUES-PIERRE

TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG

OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN

NUMBER OF SEQUENCES: 42

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/520,225

FILING DATE: 09-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 440,039

FILING DATE: 21-NOV-1989

APPLICATION NUMBER: 408,125

FILING DATE: 15-SEP-1989

SEQ ID NO:25:

LENGTH: 8

5217955-25

Query Match

Best Local Similarity 76.0%; Score 19; DB 6; Length 8;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 XXVXHL 8

Db 2 WAVGHL 7

RESULT 28

5217955-27

Patent No. 5217955

APPLICANT: ABOGDEEN, ARTHUR E.; MOREAU, JACQUES-PIERRE

TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG

OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN

NUMBER OF SEQUENCES: 42

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/520,225

FILING DATE: 09-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 440,039

FILING DATE: 21-NOV-1989

APPLICATION NUMBER: 408,125

FILING DATE: 15-SEP-1989

SEQ ID NO:27:

LENGTH: 8

5217955-27

Query Match

Best Local Similarity 76.0%; Score 19; DB 6; Length 8;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 XXVXHL 8

Db 2 WAVGHL 7

RESULT 29

5217955-28

Patent No. 5217955

APPLICANT: ABOGDEEN, ARTHUR E.; MOREAU, JACQUES-PIERRE

TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG

OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN

NUMBER OF SEQUENCES: 42

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/520,225

FILING DATE: 09-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 440,039

FILING DATE: 21-NOV-1989

APPLICATION NUMBER: 408,125

FILING DATE: 15-SEP-1989

SEQ ID NO:28:

LENGTH: 8

5217955-28

Query Match

Best Local Similarity 76.0%; Score 19; DB 6; Length 8;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 XXVXHL 8

Db 2 WAVGHL 7

RESULT 30

US-08-444-818-632

Sequence 632, Application US/08444818

Patent No. 6150087

GENERAL INFORMATION:

APPLICANT: Chien, David Y.

APPLICANT: Rutter, William J.

TITLE OF INVENTION: NANBV Diagnostics and Vaccines

NUMBER OF SEQUENCES: 777

CORRESPONDENCE ADDRESS:

ADDRESSER: Chiron Corporation

STREET: 4560 Horton Street

CITY: Emeryville

STATE: CA

COUNTRY: USA

ZIP: 94608-2916

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,818

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/403,590

FILING DATE: 14-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Harbin, Alisa A.

REGISTRATION NUMBER: 33,895

REFERENCE/DOCKET NUMBER: 0110.002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (508)359-3876

TELEFAX: (508)359-3885

INFORMATION FOR SEQ ID NO: 632:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-444-818-632

Query Match

Best Local Similarity 72.0%; Score 18; DB 3; Length 8;

Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXXVXHL 8

Db 1 RKAIVHI 7

RESULT 31

US-09-011-961-16

Sequence 16, Application US/09011961

Patent No. 6197536

GENERAL INFORMATION:

APPLICANT: STEINKUEHLER, Christian

APPLICANT: PESSI, Antonello  
APPLICANT: BIANCHI, Elisabetta  
APPLICANT: TALIANI, Marina  
APPLICANT: TOMEI, Licia  
APPLICANT: URBANI, Andrea  
APPLICANT: DE FRANCESCO, Raffaele  
APPLICANT: NARJES, Frank  
TITLE OF INVENTION: METHODOLOGY TO PRODUCE, AND PURIFY AND  
TITLE OF INVENTION: ASSAY POLYPEPTIDES WITH THE PROTEOLYTIC ACTIVITY OF THE  
TITLE OF INVENTION: HCV NS3 PROTEASE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROMDY AND NEIMARK, P.L.L.C.  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/011,961  
FILING DATE: 23-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/IT96/00163  
FILING DATE: 20-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IT RM95A000573  
FILING DATE: 22-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: STEINKUHLER=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1  
OTHER INFORMATION: /note= "Xaa is Ac-Met"  
US-09-011-961-16

Query Match 72.0%; Score 18; DB 3; Length 8;  
Best Local Similarity 37.5%; Pred. No. 3e+05;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXHL 8  
|:|:|  
Db 1 XECCASHL 8

RESULT 32  
US-09-428-082B-537  
Sequence 537, Application US/09428082B  
Patent No. 6660843  
GENERAL INFORMATION:  
APPLICANT: FEIGE, ULRICH  
APPLICANT: LIU, CHUAN-PA  
APPLICANT: CHEETHAM, JANET C.  
APPLICANT: BOONE, THOMAS CHARLES  
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
FILE REFERENCE: A-527

CURRENT APPLICATION NUMBER: US/09/428,082B  
CURRENT FILING DATE: 1999-10-22  
PRIOR APPLICATION NUMBER: 60/105,371  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 1133  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 537  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: ANTIPATHOGENIC PEPTIDE  
US-09-428-082B-537

Query Match 72.0%; Score 18; DB 4; Length 8;  
Best Local Similarity 60.0%; Pred. No. 3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 XVXHL 8  
|:|:|  
Db 1 KVFHL 5

RESULT 33  
US-09-428-082B-539  
Sequence 539, Application US/09428082B  
Patent No. 6660843  
GENERAL INFORMATION:  
APPLICANT: FEIGE, ULRICH  
APPLICANT: LIU, CHUAN-PA  
APPLICANT: CHEETHAM, JANET C.  
APPLICANT: BOONE, THOMAS CHARLES  
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
FILE REFERENCE: A-527  
CURRENT APPLICATION NUMBER: US/09/428,082B  
CURRENT FILING DATE: 1999-10-22  
PRIOR APPLICATION NUMBER: 60/105,371  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 1133  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 539  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: ANTIPATHOGENIC PEPTIDE  
US-09-428-082B-539

Query Match 72.0%; Score 18; DB 4; Length 8;  
Best Local Similarity 33.3%; Pred. No. 3e+05;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8  
|:|:|  
Db 3 FHLHL 8

RESULT 34  
US-08-427-993B-4  
Sequence 4, Application US/08427993B  
Patent No. 5668013  
GENERAL INFORMATION:  
APPLICANT: Posner, Jerome B.  
APPLICANT: FURNEAUX, Henry M.  
TITLE OF INVENTION: ANTIGEN RECOGNIZED BY PATIENTS WITH  
TITLE OF INVENTION: ANTIBODY ASSOCIATED CEREBELLAR DEGENERATION,  
TITLE OF INVENTION: DNA ENCODING SAME AND USES THEREOF  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York

COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/427,993B  
FILING DATE: April 24, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 38199-1/JPW/JKM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-427-993B-4

Query Match 68.0%; Score 17; DB 1; Length 8;  
Best Local Similarity 25.0%; Pred. No. 3e+05;  
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XOXVXVHL 8  
:|:::|  
Db 1 LQTEIANL 8

RESULT 35  
US-08-478-609A-4  
; Sequence 4, Application US/08478609A  
; Patent No. 5925526  
; GENERAL INFORMATION:  
; APPLICANT: Posner, Jerome B.  
; TITLE OF INVENTION: Furneaux, Henry M.  
; TITLE OF INVENTION: ANTIGEN RECOGNIZED BY PATIENTS WITH  
; TITLE OF INVENTION: ANTIBODY ASSOCIATED CEREBELLAR DEGENERATION,  
; TITLE OF INVENTION: DNA ENCODING SAME AND USES THEREOF  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,609A  
FILING DATE: June 5, 1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 38199-12/JPW/JKM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-478-609A-4

Query Match 68.0%; Score 17; DB 2; Length 8;  
Best Local Similarity 25.0%; Pred. No. 3e+05;  
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XOXVXVHL 8  
:|:::|  
Db 1 LQTEIANL 8

RESULT 36  
US-08-816-346-20  
; Sequence 20, Application US/08816346  
; Patent No. 6127325  
; GENERAL INFORMATION:  
; APPLICANT: Crystal, Ronald G.  
; APPLICANT: Falck-Pedersen, Erik  
; APPLICANT: Gall, Jason  
; APPLICANT: Kovacs, Imre  
; APPLICANT: Wickham, Thomas J.  
; TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND  
; TITLE OF INVENTION: METHODS OF USING SAME  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.  
; STREET: TWO PRUDENTIAL PLAZA - 4900  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: USA  
; ZIP: 60601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,346  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
REFERENCE/DOCKET NUMBER: 67167  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/616-5600  
TELEFAX: 312/616-5700  
TELEX: 25-3533  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-816-346-20

Query Match 68.0%; Score 17; DB 3; Length 8;  
Best Local Similarity 14.3%; Pred. No. 3e+05;  
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XOXVXVHL 7  
:|:::|  
Db 1 YETETINH 7

RESULT 37  
US-08-444-818-375  
Sequence 375, Application US/08444818  
Patent No. 6150087  
GENERAL INFORMATION:  
APPLICANT: Chien, David Y.  
APPLICANT: Rutter, William J.  
TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
NUMBER OF SEQUENCES: 777  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,818  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,590  
FILING DATE: 14-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Harbin, Alisha A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 0110.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508)359-3876  
TELEFAX: (508)359-3885  
INFORMATION FOR SEQ ID NO: 375:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-444-818-375

Query Match 68.0%; Score 17; DB 3; Length 8;  
Best Local Similarity 25.0%; Pred. No. 3e+05;  
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 XXXVXHL 8  
: : : : :  
DB 1 LSTGLIHL 8

RESULT 38  
US-08-444-818-633  
Sequence 633, Application US/08444818  
Patent No. 6150087  
GENERAL INFORMATION:  
APPLICANT: Chien, David Y.  
APPLICANT: Rutter, William J.  
TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
NUMBER OF SEQUENCES: 777  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,818  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,590  
FILING DATE: 14-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Harbin, Alisha A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 0110.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508)359-3876  
TELEFAX: (508)359-3885  
INFORMATION FOR SEQ ID NO: 633:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-444-818-633

Query Match 68.0%; Score 17; DB 3; Length 8;  
Best Local Similarity 33.3%; Pred. No. 3e+05;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8  
: : : : :  
DB 1 KAVTHI 6

RESULT 39  
US-09-335-411-20  
Sequence 20, Application US/09335411  
Patent No. 6153435  
GENERAL INFORMATION:  
APPLICANT: Crystal, Ronald G.  
APPLICANT: Faick-Pedersen, Erik  
APPLICANT: Gall, Jason  
APPLICANT: Kovacs, Imre  
APPLICANT: Micham, Thomas J.  
TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND  
METHODS OF USING SAME  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.  
STREET: TWO PRUDENTIAL PLAZA - 4900  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: USA  
ZIP: 60601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/335,411  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/816,346  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
REFERENCE/DOCKET NUMBER: 67167  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/616-5600  
TELEFAX: 312/616-5700  
TELEX: 25-3533  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-335-411-20

Query Match 68.0%; Score 17; DB 3; Length 8;  
Best Local Similarity 14.3%; Pred. No. 3e+05;  
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXVXH 7  
Db 1 YETELNH 7

RESULT 40  
US-09-515-965A-1889  
Sequence 1889, Application US/09515965A  
Patent No. 6623741  
GENERAL INFORMATION:  
APPLICANT: Antczak, J.  
APPLICANT: Delmedico, M.  
APPLICANT: Erickson, J.  
APPLICANT: Lambert, D.  
APPLICANT: Sista, P.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-  
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION  
FILE REFERENCE: 7872-073  
CURRENT APPLICATION NUMBER: US/09/515,965A  
CURRENT FILING DATE: 2000-02-29  
PRIOR APPLICATION NUMBER: 09/315,304  
PRIOR FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1994  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1889  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-515-965A-1889

Query Match 68.0%; Score 17; DB 4; Length 8;  
Best Local Similarity 75.0%; Pred. No. 3e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 VXLH 8  
Db 1 VLHL 4

RESULT 41  
US-07-872-644-34  
Sequence 34, Application US/07872644  
Patent No. 5389527  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA

ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/872,644  
FILING DATE: 19920420  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5389527and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-872-644-34

Query Match 64.0%; Score 16; DB 1; Length 8;  
Best Local Similarity 14.3%; Pred. No. 3e+05;  
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 OXXVXHL 8  
Db 1 EMMNTM 7

RESULT 42  
US-08-297-494-34  
Sequence 34, Application US/08297494  
Patent No. 5580771  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,494  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5580771and, Greta E.

REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-297-494-34

Query Match 64.0%; Score 16; DB 1; Length 8;  
Best Local Similarity 14.3%; Pred. No. 3e+05;  
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXXVXHL 8  
Db 1 EMMMYHM 7

RESULT 43  
US-08-297-510-34  
Sequence 34, Application US/08297510  
Patent No. 5602019

GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonenbourg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,510  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5602019and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-297-510-34

Query Match 64.0%; Score 16; DB 1; Length 8;

Best Local Similarity 14.3%; Pred. No. 3e+05;  
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXXVXHL 8  
Db 1 EMMMYHM 7

RESULT 44  
US-08-479-532-34  
Sequence 34, Application US/08479532  
Patent No. 576752  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonenbourg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,532  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/297,494  
FILING DATE:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 576752and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-479-532-34

Query Match 64.0%; Score 16; DB 1; Length 8;  
Best Local Similarity 14.3%; Pred. No. 3e+05;  
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXXVXHL 8  
Db 1 EMMMYHM 7

RESULT 45  
US-08-571-985-22  
Sequence 22, Application US/08571985  
Patent No. 578357  
GENERAL INFORMATION:

APPLICANT: Birstein, Yigal  
APPLICANT: Trainin, Nathan  
APPLICANT: Rycus, Avigal  
TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical  
TITLE OF INVENTION: Compositions Comprising Them  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kohn & Associates  
STREET: 30500 No. 578357thwestern Hwy., Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: USA  
ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/571,985  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 106214  
FILING DATE: 01-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: 2163.00048  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (810) 539-5050  
TELEFAX: (810) 539-5055  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-571-985-22

Query Match 64.0%; Score 16; DB 1; Length 8;  
Best Local Similarity 25.0%; Pred. No. 3e+05;  
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 1 XQXXVXHL 8  
Db 1 LEDGPKHL 8

Search completed: August 19, 2004, 15:52:27  
Job time : 14.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 19, 2004, 15:51:28 ; Search time 38 Seconds  
(without alignments)  
66.159 Million cell updates/sec

Title: VARIANT1  
Perfect score: 25  
Sequence: 1 XXXVXHL 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 31425058 residues

Total number of hits satisfying chosen parameters: 16665

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	8	10	US-09-896-903C-2
2	25	100.0	8	14	US-10-186-226A-2
3	25	100.0	8	16	US-10-329-321A-2
4	24	96.0	8	9	US-09-766-347-1
5	24	96.0	8	10	US-09-898-887B-1
6	24	96.0	8	14	US-10-281-840-2
7	24	96.0	8	16	US-10-341-577-1
8	21	84.0	8	14	US-10-004-530A-4
9	19	76.0	8	12	US-10-182-252A-332
10	19	76.0	8	12	US-10-182-252A-940
11	19	76.0	8	12	US-10-182-252A-941
12	19	76.0	8	12	US-10-182-252A-942
13	19	76.0	8	12	US-10-182-252A-943
14	19	76.0	8	12	US-10-182-252A-944
15	19	76.0	8	12	US-10-182-252A-946

16	19	76.0	8	12	US-10-182-252A-947	Sequence 947, App
17	19	76.0	8	12	US-10-182-252A-948	Sequence 948, App
18	19	76.0	8	12	US-10-182-252A-950	Sequence 950, App
19	19	76.0	8	12	US-10-182-252A-951	Sequence 951, App
20	19	76.0	8	12	US-10-182-252A-1285	Sequence 1285, App
21	18	72.0	8	9	US-09-899-422-28	Sequence 28, App1
22	18	72.0	8	9	US-09-898-234-38	Sequence 28, App1
23	18	72.0	8	9	US-09-899-429A-38	Sequence 38, App1
24	18	72.0	8	9	US-09-017-743C-100	Sequence 100, App
25	18	72.0	8	9	US-09-792-156-28	Sequence 28, App1
26	18	72.0	8	12	US-10-609-217-537	Sequence 537, App
27	18	72.0	8	12	US-10-609-217-539	Sequence 539, App
28	18	72.0	8	12	US-10-149-135-36	Sequence 36, App1
29	18	72.0	8	12	US-10-149-135-116	Sequence 116, App
30	18	72.0	8	12	US-10-149-135-313	Sequence 313, App
31	18	72.0	8	12	US-10-149-135-549	Sequence 549, App
32	18	72.0	8	12	US-10-149-135-649	Sequence 649, App
33	18	72.0	8	12	US-10-149-135-674	Sequence 674, App
34	18	72.0	8	12	US-10-149-135-808	Sequence 808, App
35	18	72.0	8	12	US-10-149-135-818	Sequence 818, App
36	18	72.0	8	12	US-10-149-135-1175	Sequence 1175, App
37	18	72.0	8	12	US-10-149-135-1180	Sequence 1180, App
38	18	72.0	8	12	US-10-149-135-1192	Sequence 1192, App
39	18	72.0	8	12	US-10-149-135-1487	Sequence 1487, App
40	18	72.0	8	12	US-10-149-135-1651	Sequence 1651, App
41	18	72.0	8	12	US-10-149-135-1763	Sequence 1763, App
42	18	72.0	8	12	US-10-149-135-1854	Sequence 1854, App
43	18	72.0	8	12	US-10-149-135-2451	Sequence 2451, App
44	18	72.0	8	12	US-10-387-957-6	Sequence 6, App11
45	18	72.0	8	12	US-10-632-388-537	Sequence 537, App

## ALIGNMENTS

RESULT 1  
US-09-896-903C-2  
; Publication No. US20030050233A1  
; GENERAL INFORMATION:  
; APPLICANT: Burman, Anand C.  
; APPLICANT: Mukherjee, Rama  
; APPLICANT: Prasad, Sudhanand  
; APPLICANT: Jaggi, Manu  
; APPLICANT: Singh, Anu T.  
; TITLE OF INVENTION: PEPTIDE COMBINATION FOR TREATMENT OF CANCER  
; FILE REFERENCE: 0132970  
; CURRENT APPLICATION NUMBER: US/09/896,903C  
; CURRENT FILING DATE: 2001-06-29  
; NUMBER OF SEQ. ID NOS.: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: This peptide  
; OTHER INFORMATION: was synthetically generated.  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: /product = Butanoyl D-phenylalanine/label =  
; OTHER INFORMATION: Butanoyl-D-phe  
; NAME/KEY: MOD\_RES  
; LOCATION: (6)  
; OTHER INFORMATION: / product = alpha-Aminoisobutyric acid/label = Alb  
US-09-896-903C-2  
Query Match 100.0%; Score 25; DB 10; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHL 8  
|:|:|:|  
DB 1 XQWAVXHL 8

## RESULT 2

US-10-186-226A-2  
; Sequence 2, Application US/10186226A  
; Publication No. US20030105009A1  
; GENERAL INFORMATION:  
; APPLICANT: Prasad, Sudhanand  
; APPLICANT: Mukherjee, Rama  
; APPLICANT: Burman, Anand C.  
; APPLICANT: Mathur, Archana  
; APPLICANT: Sharma, Rajan  
; APPLICANT: Jaggi, Manu  
; TITLE OF INVENTION: POLYPEPTIDES OF COVALENTLY LINKED SYNTHETIC BIOACTIVE PEPTIDE ANA  
; TITLE OF INVENTION: FOR TREATMENT OF CANCER  
; FILE REFERENCE: U 014073-7  
; CURRENT APPLICATION NUMBER: US/10/186,226A  
; CURRENT FILING DATE: 2002-08-16  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: This peptide was synthetically generated  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: /product = D-Phenylalanine/label = D-Phe  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (6)..(6)  
; OTHER INFORMATION: /product = Alpha-amino-isobutyric acid/label = Alb  
US-10-186-226A-2

Query Match 100.0%; Score 25; DB 14; Length 8;  
Best local Similarity 75.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHL 8  
|:|:|:|  
DB 1 XQWAVXHL 8

## RESULT 3

US-10-329-321A-2  
; Sequence 2, Application US/10329321A  
; Publication No. US20040121950A1  
; GENERAL INFORMATION:  
; APPLICANT: Mukherjee, Rama  
; APPLICANT: Burman, Anand  
; APPLICANT: Singh, Anu  
; APPLICANT: Jaggi, Manu  
; APPLICANT: Prasad, Sudhanand  
; APPLICANT: Dutt, Sarjana  
; TITLE OF INVENTION: A DRUG COMPRISING SYNTHETIC PEPTIDE ANALOGS FOR THE TREATMENT OF  
; TITLE OF INVENTION: CANCER  
; FILE REFERENCE: U 014319-1  
; CURRENT APPLICATION NUMBER: US/10/329,321A  
; CURRENT FILING DATE: 2002-12-23  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: This peptide was synthetically generated  
; FEATURE:

; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: /product = D-phenylalanine/label = D-Phe  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (6)..(6)  
; OTHER INFORMATION: /product = 2-amino-isobutyric acid/label = Alb  
US-10-329-321A-2

Query Match 100.0%; Score 25; DB 16; Length 8;  
Best local Similarity 75.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXHL 8  
|:|:|:|  
DB 1 XQWAVXHL 8

## RESULT 4

US-09-766-347-1  
; Sequence 1, Application US/09766347  
; Patent No. US20020169107A1  
; GENERAL INFORMATION:  
; APPLICANT: Rajagopalan, Raghavan  
; APPLICANT: Cantrell, Gary  
; APPLICANT: Achilefu, Samuel  
; APPLICANT: Bugaj, Joseph  
; APPLICANT: Dorehow, Richard  
; APPLICANT: Mallinckrodt Inc.  
; TITLE OF INVENTION: NOVEL AROMATIC AZIDES FOR TYPE I PHOTOTHERAPY  
; FILE REFERENCE: MRD-60  
; CURRENT APPLICATION NUMBER: US/09/766,347  
; CURRENT FILING DATE: 2001-01-19  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: Patent In Version 3.1  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: Bombesin analog  
US-09-766-347-1

Query Match 96.0%; Score 24; DB 9; Length 8;  
Best local Similarity 57.1%; Pred. No. 1.2e+06;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXHL 8  
|:|:|:|  
DB 1 QWAVGHL 7

## RESULT 5

US-09-898-887B-1  
; Sequence 1, Application US/09898887B  
; Publication No. US20030158127A1  
; GENERAL INFORMATION:  
; APPLICANT: Mallinckrodt Inc.  
; APPLICANT: Rajagopalan, Raghavan  
; APPLICANT: Cantrell, Gary  
; APPLICANT: Achilefu, Samuel I.  
; APPLICANT: Bugaj, Joseph  
; APPLICANT: Dorehow, Richard  
; TITLE OF INVENTION: AROMATIC SULFONATES FOR TYPE I PHOTOTHERAPY  
; FILE REFERENCE: MRD-61  
; CURRENT APPLICATION NUMBER: US/09/898,887B  
; CURRENT FILING DATE: 2001-07-03  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 8

;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: The sulfenato-bombesin (7-14) conjugate has the following  
;; OTHER INFORMATION: molecular structure:  
;; OTHER INFORMATION: p-azidotetrafluorobenzoyl-Gln-Trp-Ala-Val-Gly-His-Leu-Met-NH2.  
US-09-898-887B-1

Query Match                    96.0%; Score 24; DB 10; Length 8;  
Best Local Similarity    57.1%; Pred. No. 1.2e+06;  
Matches    4; Conservative    3; Mismatches    0; Indels    0; Gaps    0;

QY                    2 QXXVXHL 8  
                      |:::|  
DB                    1 QMAVGH 7

RESULT 6  
US-10-281-840-2  
; Sequence 2, Application US/10281840  
; Publication No. US20030082192A1  
; GENERAL INFORMATION:  
; APPLICANT: Safavy, Ahmad  
; TITLE OF INVENTION: Multidrug Multiligand Conjugates for Targeted Drug Delivery  
; FILE REFERENCE: P66788US01GP  
; CURRENT APPLICATION NUMBER: US/10/281,840  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US 60/348,299  
; PRIOR FILING DATE: 2001-10-26  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-281-840-2

Query Match                    96.0%; Score 24; DB 14; Length 8;  
Best Local Similarity    57.1%; Pred. No. 1.2e+06;  
Matches    4; Conservative    3; Mismatches    0; Indels    0; Gaps    0;

QY                    2 QXXVXHL 8  
                      |:::|  
DB                    1 QMAVGH 7

RESULT 7  
US-10-341-577-1  
; Sequence 1, Application US/10341577  
; Publication No. US20040136906A1  
; GENERAL INFORMATION:  
; APPLICANT: Bracco Research U.S.A.  
; TITLE OF INVENTION: Improved Gastrin Releasing Peptide Compounds  
; FILE REFERENCE: 57637-1020  
; CURRENT APPLICATION NUMBER: US/10/341,577  
; CURRENT FILING DATE: 2003-01-13  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: This peptide is the receptor  
; OTHER INFORMATION: binding site of Bombesin and is also known as BBN(7-14)  
US-10-341-577-1

Query Match                    96.0%; Score 24; DB 16; Length 8;  
Best Local Similarity    57.1%; Pred. No. 1.2e+06;  
Matches    4; Conservative    3; Mismatches    0; Indels    0; Gaps    0;

QY                    2 QXXVXHL 8  
                      |:::|

DB                    1 QMAVGH 7

RESULT 8  
US-10-004-530A-4  
; Sequence 4, Application US/10004530A  
; Publication No. US20030050436A1  
; GENERAL INFORMATION:  
; APPLICANT: Coy, David H.  
; APPLICANT: Moreau, Jacques-Pierre  
; APPLICANT: Kim, Sun H.  
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS  
; FILE REFERENCE: 00537-00900K  
; CURRENT APPLICATION NUMBER: US/10/004,530A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 09/260,846  
; PRIOR FILING DATE: 1999-03-02  
; PRIOR APPLICATION NUMBER: 08/337,127  
; PRIOR FILING DATE: 1994-11-10  
; PRIOR APPLICATION NUMBER: 07/779,039  
; PRIOR FILING DATE: 1991-10-18  
; PRIOR APPLICATION NUMBER: 07/502,438  
; PRIOR FILING DATE: 1990-03-30  
; PRIOR APPLICATION NUMBER: 07/397,169  
; PRIOR FILING DATE: 1989-08-21  
; PRIOR APPLICATION NUMBER: 07/376,555  
; PRIOR FILING DATE: 1989-07-07  
; PRIOR APPLICATION NUMBER: 07/317,941  
; PRIOR FILING DATE: 1989-03-02  
; PRIOR APPLICATION NUMBER: 07/282,328  
; PRIOR FILING DATE: 1988-12-09  
; PRIOR APPLICATION NUMBER: 07/257,998  
; PRIOR FILING DATE: 1988-10-14  
; PRIOR APPLICATION NUMBER: 07/248,771  
; PRIOR FILING DATE: 1988-09-23  
; Prior Application data removed - See file wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated peptide  
; NAME/KEY: VARIANT  
; LOCATION: 8  
; OTHER INFORMATION: Xaa = statine;  
US-10-004-530A-4

Query Match                    84.0%; Score 21; DB 14; Length 8;  
Best Local Similarity    42.9%; Pred. No. 1.2e+06;  
Matches    3; Conservative    4; Mismatches    0; Indels    0; Gaps    0;

QY                    1 QXXVXHL 7  
                      |:::|  
DB                    1 EQMAVGH 7

RESULT 9  
US-10-182-252A-322  
; Sequence 322, Application US/10182252A  
; Publication No. US20040072162A1  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; APPLICANT: BRUNAK, SOREN  
; APPLICANT: BUS, SOREN  
; APPLICANT: CORBET, SYLVIE  
; APPLICANT: LAUEMOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; FILE REFERENCE: 030307/0205

```
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: Patentin Ver. 2.1
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-322
```

```
Query Match      76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db      1 QIGIPH 6
```

```
RESULT 10
US-10-182-252A-940
/ Sequence 940, Application US/10182252A
/ Publication No. US20040072162A1
/ GENERAL INFORMATION:
/ APPLICANT: FOMSGAARD, ANDERS
/ APPLICANT: BRUNAK, SOREN
/ APPLICANT: BUTS, SOREN
/ APPLICANT: CORBET, SYLVIE
/ APPLICANT: LAUEMOLLER, SANNE LISE
/ APPLICANT: HANSEN, JAN
/ TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
/ FILE REFERENCE: 030307/0205
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: Patentin Ver. 2.1
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-940
```

```
Query Match      76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db      1 QIGIPH 6
```

```
RESULT 11
US-10-182-252A-941
/ Sequence 941, Application US/10182252A
/ Publication No. US20040072162A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: FOMSGAARD, ANDERS
/ APPLICANT: BRUNAK, SOREN
/ APPLICANT: BUTS, SOREN
/ APPLICANT: CORBET, SYLVIE
/ APPLICANT: LAUEMOLLER, SANNE LISE
/ APPLICANT: HANSEN, JAN
/ TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
/ FILE REFERENCE: 030307/0205
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: Patentin Ver. 2.1
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-941
```

```
Query Match      76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db      1 QIGIPH 6
```

```
RESULT 12
US-10-182-252A-942
/ Sequence 942, Application US/10182252A
/ Publication No. US20040072162A1
/ GENERAL INFORMATION:
/ APPLICANT: FOMSGAARD, ANDERS
/ APPLICANT: BRUNAK, SOREN
/ APPLICANT: BUTS, SOREN
/ APPLICANT: CORBET, SYLVIE
/ APPLICANT: LAUEMOLLER, SANNE LISE
/ APPLICANT: HANSEN, JAN
/ TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
/ FILE REFERENCE: 030307/0205
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: Patentin Ver. 2.1
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-942
```

```
Query Match      76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
```

Db 1 QIGIPH 6

RESULT 13

US-10-182-252A-943  
 ; Sequence 943, Application US/10182252A  
 ; Publication No. US20040072162A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FOMSGAARD, ANDERS  
 ; APPLICANT: BRUNAK, SOREN  
 ; APPLICANT: BUIS, SOREN  
 ; APPLICANT: CORBET, SYLVIE  
 ; APPLICANT: LAUEMOLLER, SANNE LISE  
 ; APPLICANT: HANSEN, JAN  
 ; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
 ; FILE REFERENCE: 030307/0205  
 ; CURRENT APPLICATION NUMBER: US/10/182,252A  
 ; PRIOR FILING DATE: 2003-04-10  
 ; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
 ; PRIOR FILING DATE: 2001-01-29  
 ; PRIOR APPLICATION NUMBER: EP 00610017.6  
 ; PRIOR FILING DATE: 2000-01-28  
 ; PRIOR APPLICATION NUMBER: US 60/179,333  
 ; PRIOR FILING DATE: 2000-01-31  
 ; NUMBER OF SEQ ID NOS: 1388  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 943  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
 US-10-182-252A-943

Query Match 76.0%; Score 19; DB 12; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7  
 Db 1 QIGIPH 6

RESULT 14  
 US-10-182-252A-944  
 ; Sequence 944, Application US/10182252A  
 ; Publication No. US20040072162A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FOMSGAARD, ANDERS  
 ; APPLICANT: BRUNAK, SOREN  
 ; APPLICANT: BUIS, SOREN  
 ; APPLICANT: CORBET, SYLVIE  
 ; APPLICANT: LAUEMOLLER, SANNE LISE  
 ; APPLICANT: HANSEN, JAN  
 ; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
 ; FILE REFERENCE: 030307/0205  
 ; CURRENT APPLICATION NUMBER: US/10/182,252A  
 ; PRIOR FILING DATE: 2003-04-10  
 ; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
 ; PRIOR FILING DATE: 2001-01-29  
 ; PRIOR APPLICATION NUMBER: EP 00610017.6  
 ; PRIOR FILING DATE: 2000-01-28  
 ; PRIOR APPLICATION NUMBER: US 60/179,333  
 ; PRIOR FILING DATE: 2000-01-31  
 ; NUMBER OF SEQ ID NOS: 1388  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 944  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence

FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
 US-10-182-252A-944

Query Match 76.0%; Score 19; DB 12; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7  
 Db 1 QIGIPH 6

RESULT 15  
 US-10-182-252A-946  
 ; Sequence 946, Application US/10182252A  
 ; Publication No. US20040072162A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FOMSGAARD, ANDERS  
 ; APPLICANT: BRUNAK, SOREN  
 ; APPLICANT: BUIS, SOREN  
 ; APPLICANT: CORBET, SYLVIE  
 ; APPLICANT: LAUEMOLLER, SANNE LISE  
 ; APPLICANT: HANSEN, JAN  
 ; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
 ; FILE REFERENCE: 030307/0205  
 ; CURRENT APPLICATION NUMBER: US/10/182,252A  
 ; PRIOR FILING DATE: 2003-04-10  
 ; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
 ; PRIOR FILING DATE: 2001-01-29  
 ; PRIOR APPLICATION NUMBER: EP 00610017.6  
 ; PRIOR FILING DATE: 2000-01-28  
 ; PRIOR APPLICATION NUMBER: US 60/179,333  
 ; PRIOR FILING DATE: 2000-01-31  
 ; NUMBER OF SEQ ID NOS: 1388  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 946  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
 US-10-182-252A-946

Query Match 76.0%; Score 19; DB 12; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7  
 Db 1 QIGIPH 6

RESULT 16  
 US-10-182-252A-947  
 ; Sequence 947, Application US/10182252A  
 ; Publication No. US20040072162A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FOMSGAARD, ANDERS  
 ; APPLICANT: BRUNAK, SOREN  
 ; APPLICANT: BUIS, SOREN  
 ; APPLICANT: CORBET, SYLVIE  
 ; APPLICANT: LAUEMOLLER, SANNE LISE  
 ; APPLICANT: HANSEN, JAN  
 ; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
 ; FILE REFERENCE: 030307/0205  
 ; CURRENT APPLICATION NUMBER: US/10/182,252A  
 ; PRIOR FILING DATE: 2003-04-10  
 ; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
 ; PRIOR FILING DATE: 2001-01-29  
 ; PRIOR APPLICATION NUMBER: EP 00610017.6

```
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 947
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-947
```

```
Query Match          76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db      1 QMGIPH 6
```

```
RESULT 17
US-10-182-252A-948
; Sequence 948, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BRUNAK, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEWOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 948
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-948
```

```
Query Match          76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db      1 QMGIPH 6
```

```
RESULT 18
US-10-182-252A-950
; Sequence 950, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BRUNAK, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEWOLLER, SANNE LISE
```

```
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 950
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-950
```

```
Query Match          76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db      1 QMGIPH 6
```

```
RESULT 19
US-10-182-252A-951
; Sequence 951, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BRUNAK, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEWOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 951
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-951
```

```
Query Match          76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
        |:::|
Db      1 QMGIPH 6
```

RESULT 20

```

US-10-182-252A-1285
: Sequence 1285, Application US/10182252A
: Publication No. US20040072162A1
: GENERAL INFORMATION:
: APPLICANT: FOMSGAARD, ANDERS
: APPLICANT: BRUNAK, SOREN
: APPLICANT: BUUS, SOREN
: APPLICANT: CORREBT, SYLVIE
: APPLICANT: LADEMOLLER, SANNE LISE
: APPLICANT: HANSEN, JAN
: TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
: TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
: FILE REFERENCE: 030307/0205
: CURRENT APPLICATION NUMBER: US/10/182,252A
: CURRENT FILING DATE: 2003-04-10
: PRIOR APPLICATION NUMBER: PCT/DK01/00059
: PRIOR FILING DATE: 2001-01-29
: PRIOR APPLICATION NUMBER: EP 00610017.6
: PRIOR FILING DATE: 2000-01-28
: PRIOR APPLICATION NUMBER: US 60/179,333
: PRIOR FILING DATE: 2000-01-31
: NUMBER OF SEQ ID NOS: 1388
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1285
:
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Human immunodeficiency virus
US-10-182-252A-1285

```

```

Query Match 76.0% Score 19 DB 12 Length 8
Best Local Similarity 33.3% Pred No 1.2e+06
Matches 2 Conservative 4 Mismatches 0 Gaps 0

```

QY	2	QXXVXH	7
		:::	
Db	1	QLGIPH	6

RESULT 21  
 US-09-899-422-28  
 : Sequence 28 'Application US/09899422  
 : Patent No. 'US20020090676A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Hauptmann, Rudolph  
 : APPLICANT: Himmler, Adolph  
 : APPLICANT: Maurer-Foggy, Ingrid  
 : APPLICANT: Stratowa, Christian  
 : TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
 : TITLE OF INVENTION: Them  
 : FILE REFERENCE: 98,385-H  
 : CURRENT APPLICATION NUMBER: US/09/899,422  
 : CURRENT FILING DATE: 2001-08-21  
 : PRIOR APPLICATION NUMBER: 09/525,998  
 : PRIOR FILING DATE: 2000-03-15  
 : PRIOR APPLICATION NUMBER: 08/383,676  
 : PRIOR FILING DATE: 1995-02-01  
 : PRIOR APPLICATION NUMBER: 08/453,287  
 : PRIOR FILING DATE: 1993-11-17  
 : PRIOR APPLICATION NUMBER: 07/821,750  
 : PRIOR FILING DATE: 1992-01-02  
 : PRIOR APPLICATION NUMBER: 07/511,430  
 : PRIOR FILING DATE: 1990-04-20  
 : NUMBER OF SEQ ID NOS: 87  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 28  
 : LENGTH: 8  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Description of Artificial Sequence: TNF-BP tryptic  
 : US-09-899-422-28

Query Match	72.0%	Score 18;	DB 9;	Length 8;
Best Local Similarity	60.0%	Pred. No. 1.2e+06;		
Matches	3;	Conservative	2;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	4	XVXHL	8	
	:	:	:	
DB	1	LVPHL	5	

```

RESULT 22
US-09-898-234-28
; Sequence 28, Application US/090898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stralowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNA Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,267
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TNF-BP tryptic
; OTHER INFORMATION: cleavage peptide
US-09-898-234-28
|
Query Match          72.0%  Score 18; DB 9; Length 8;
Best Local Similarity 60.0%  Pred. No. 1.2e+06;
Matches      3; Conservative      2; Mismatches      0; Indels      0;
|
Oy      4  XVXHL 8
      :  |||
Db      1  LVPHL 5
      :

```

```

RESULT 23
US-09-899-429A-38
; Sequence 38, Application US/09899429A
; Patent No. US20020169118A1
GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Fogt, Ingrid
; APPLICANT: Strelova, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01

```

PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 38  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: TNF-BP tryptic  
OTHER INFORMATION: cleavage peptide  
US-09-429A-38

Query Match  
Best Local Similarity 72.0%; Score 18; DB 9; Length 8;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 XYVXL 8  
:|:|  
DB 1 LVPHL 5

RESULT 24  
US-09-017-743C-100  
Sequence 100, Application US/09017743C  
Patent No. US20020177694A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
Sidney, John  
Southwood, Scott  
TITLE OF INVENTION: HLA Binding Peptides and Their  
Uses  
NUMBER OF SEQUENCES: 146  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/017,743C  
FILING DATE: 03-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/590,298  
FILING DATE: 23-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Parent, Annette S.  
REGISTRATION NUMBER: 42,058  
REFERENCE/DOCKET NUMBER: 018623-008050US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 100:  
US-09-017-743C-100

Query Match  
Best Local Similarity 72.0%; Score 18; DB 9; Length 8;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XYVXL 8  
:|:|  
DB 1 LVPHL 6

RESULT 25  
US-09-792-356-28  
Sequence 28, Application US/09792356  
Publication No. US20020183485A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
Himmeler, Adolf  
APPLICANT: Maurer-Fosy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
Them  
FILE REFERENCE: 98,385-G  
CURRENT APPLICATION NUMBER: US/09/792,356  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 28  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: TNF-BP tryptic  
OTHER INFORMATION: cleavage peptide  
US-09-792-356-28

Query Match  
Best Local Similarity 72.0%; Score 18; DB 9; Length 8;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 XYVXL 8  
:|:|  
DB 1 LVPHL 5

RESULT 26  
US-10-609-217-537  
Sequence 537, Application US/10609217  
Publication No. US20040044188A1  
GENERAL INFORMATION:  
APPLICANT: FEIGE, ULRICH  
APPLICANT: LIU, CHUAN-FA  
APPLICANT: CHEETHAM, JANET C.  
APPLICANT: BOONE, THOMAS CHARLES  
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
FILE REFERENCE: A-527  
CURRENT APPLICATION NUMBER: US/10/609,217  
CURRENT FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: US/09/428,082B  
PRIOR FILING DATE: 1999-10-22  
PRIOR APPLICATION NUMBER: 60/105,371  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 1133  
SOFTWARE: Patentin version 3.1



SEQ ID NO 537  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: ANTIPATHOGENIC PEPTIDE  
US-10-609-217-537

Query Match 72.0%; Score 18; DB 12; Length 8;  
Best Local Similarity 60.0%; Pred. No. 1.2e+06;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 XXVXHL 8  
:|:|:  
Db 1 KVFHL 5

RESULT 27  
US-10-609-217-539  
Sequence 539, Application US/10609217  
Publication No. US20040044188A1  
GENERAL INFORMATION:  
APPLICANT: FEIGE, ULRICH  
APPLICANT: LIU, CHUAN-PA  
APPLICANT: CHEETHAM, JANET C.  
APPLICANT: BOONE, THOMAS CHARLES  
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
FILE REFERENCE: A-527  
CURRENT APPLICATION NUMBER: US/10/609,217  
CURRENT FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: US/09/428,082B  
PRIOR FILING DATE: 1999-10-22  
PRIOR APPLICATION NUMBER: 60/105,371  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 1133  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 539  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: ANTIPATHOGENIC PEPTIDE  
US-10-609-217-539

Query Match 72.0%; Score 18; DB 12; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8  
:|:|:  
Db 3 FHLHL 8

RESULT 28  
US-10-149-135-36  
Sequence 36, Application US/10149135  
Publication No. US20040053822A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Eateban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060 0130001  
CURRENT APPLICATION NUMBER: US/10/149,135  
CURRENT FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: PCT/US00/33545  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,298

PRIOR FILING DATE: 1999-12-10  
PRIOR APPLICATION NUMBER: US 09/189,702  
PRIOR FILING DATE: 1998-11-10  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
NUMBER OF SEQ ID NOS: 2479  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 36  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial Peptide  
US-10-149-135-36

Query Match 72.0%; Score 18; DB 12; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8  
:|:|:  
Db 2 VPLSHL 7

RESULT 29  
US-10-149-135-116  
Sequence 116, Application US/10149135  
Publication No. US20040053822A1  
GENERAL INFORMATION:  
APPLICANT: Fikes, John  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Celis, Eateban  
APPLICANT: Keogh, Elissa  
TITLE OF INVENTION: Inducing Cellular Immune Responses to  
FILE REFERENCE: 2060 0130001  
CURRENT APPLICATION NUMBER: US/10/149,135  
CURRENT FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: PCT/US00/33545  
PRIOR FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 09/458,298  
PRIOR FILING DATE: 1999-12-10  
PRIOR APPLICATION NUMBER: US 09/189,702  
PRIOR FILING DATE: 1998-11-10  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
NUMBER OF SEQ ID NOS: 2479  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 116  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial Peptide  
US-10-149-135-116

Query Match 72.0%; Score 18; DB 12; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.2e+06;

Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVXHL 8  
Db 3 VPISHL 8

RESULT 30  
US-10-149-135-313  
; Sequence 313, Application US/10149135  
; Publication No. US20040053822A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions  
; CURRENT FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US/10/149,135  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: PCT/US00/33545  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,298  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: US 09/189,702  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: US 08/205,713  
; PRIOR FILING DATE: 1994-03-04  
; PRIOR APPLICATION NUMBER: US 08/159,184  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/073,205  
; PRIOR FILING DATE: 1993-06-04  
; PRIOR APPLICATION NUMBER: US 08/027,146  
; PRIOR FILING DATE: 1993-03-05  
; NUMBER OF SEQ ID NOS: 2479  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 313  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide  
US-10-149-135-313

Query Match 72.0%; Score 18; DB 12; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVXHL 8  
Db 3 DPIGHL 8

RESULT 31  
US-10-149-135-549  
; Sequence 549, Application US/10149135  
; Publication No. US20040053822A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions  
; CURRENT APPLICATION NUMBER: US/10/149,135

CURRENT FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: PCT/US00/33545  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,298  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: US 09/189,702  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: US 08/205,713  
; PRIOR FILING DATE: 1994-03-04  
; PRIOR APPLICATION NUMBER: US 08/159,184  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/073,205  
; PRIOR FILING DATE: 1993-06-04  
; PRIOR APPLICATION NUMBER: US 08/027,146  
; PRIOR FILING DATE: 1993-03-05  
; NUMBER OF SEQ ID NOS: 2479  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 549  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide  
US-10-149-135-549

Query Match 72.0%; Score 18; DB 12; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVXHL 8  
Db 3 VPISHL 8

RESULT 32  
US-10-149-135-649  
; Sequence 649, Application US/10149135  
; Publication No. US20040053822A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions  
; CURRENT APPLICATION NUMBER: US/10/149,135  
; CURRENT FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: PCT/US00/33545  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,298  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: US 09/189,702  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: US 08/205,713  
; PRIOR FILING DATE: 1994-03-04  
; PRIOR APPLICATION NUMBER: US 08/159,184  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/073,205  
; PRIOR FILING DATE: 1993-06-04  
; PRIOR APPLICATION NUMBER: US 08/027,146  
; PRIOR FILING DATE: 1993-03-05  
; NUMBER OF SEQ ID NOS: 2479  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 649  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide

US-10-149-135-649

Query Match 72.0%; Score 18; DB 12; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVXHL 8  
: : : :  
DB 2 VPISHL 7

RESULT 33

US-10-149-135-674  
Sequence 674, Application US/10149135  
Publication No. US20040053822A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Keogh, Eلسga

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0130001

CURRENT APPLICATION NUMBER: US/10/149,135

CURRENT FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: PCT/US00/33545

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,298

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US 09/189,702

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04

PRIOR APPLICATION NUMBER: US 08/159,184

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/073,205

PRIOR FILING DATE: 1993-06-04

PRIOR APPLICATION NUMBER: US 08/027,146

PRIOR FILING DATE: 1993-03-05

NUMBER OF SEQ ID NOS: 2479

SOFTWARE: PatentIn version 3.1

SEQ ID NO 674

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificial Peptide

US-10-149-135-674

Query Match 72.0%; Score 18; DB 12; Length 8;

Best Local Similarity 33.3%; Pred. No. 1.2e+06;

Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVXHL 8  
: : : :  
DB 3 DPIGHL 8

RESULT 34

US-10-149-135-808

Sequence 808, Application US/10149135

Publication No. US20040053822A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Keogh, Eلسga

APPLICANT: Keogh, Eلسga

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0130001

CURRENT APPLICATION NUMBER: US/10/149,135

CURRENT FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: PCT/US00/33545

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,298

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US 09/189,702

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04

PRIOR APPLICATION NUMBER: US 08/159,184

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/073,205

PRIOR FILING DATE: 1993-06-04

PRIOR APPLICATION NUMBER: US 08/027,146

PRIOR FILING DATE: 1993-03-05

NUMBER OF SEQ ID NOS: 2479

SOFTWARE: PatentIn version 3.1

SEQ ID NO 808

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Artificial Peptide

US-10-149-135-808

Query Match 72.0%; Score 18; DB 12; Length 8;

Best Local Similarity 33.3%; Pred. No. 1.2e+06;

Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVXHL 8  
: : : :  
DB 1 VPISHL 6

RESULT 35

US-10-149-135-818

Sequence 818, Application US/10149135

Publication No. US20040053822A1

GENERAL INFORMATION:

APPLICANT: Fikes, John

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Keogh, Eلسga

TITLE OF INVENTION: Inducing Cellular Immune Responses to

FILE REFERENCE: 2060.0130001

CURRENT APPLICATION NUMBER: US/10/149,135

CURRENT FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: PCT/US00/33545

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,298

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US 09/189,702

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04

PRIOR APPLICATION NUMBER: US 08/159,184

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/073,205

PRIOR FILING DATE: 1993-06-04

PRIOR APPLICATION NUMBER: US 08/027,146

PRIOR FILING DATE: 1993-03-05

NUMBER OF SEQ ID NOS: 2479

SOFTWARE: PatentIn version 3.1

SEQ ID NO 818

LENGTH: 8

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-818

Query Match
Best Local Similarity 72.0%; Score 18; DB 12; Length 8;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
Db 1 DPIGHL 6

RESULT 36
US-10-149-135-1175
; Sequence 1175, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esleben
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1175
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1175

Query Match
Best Local Similarity 72.0%; Score 18; DB 12; Length 8;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
Db 1 VPISHL 6

RESULT 37
US-10-149-135-1180
; Sequence 1180, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
```

```
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esleben
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1180
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1180

Query Match
Best Local Similarity 72.0%; Score 18; DB 12; Length 8;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
Db 2 VPISHL 7

RESULT 38
US-10-149-135-1192
; Sequence 1192, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esleben
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
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; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1192
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1192

Query Match      72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 XXVXHL 8
       :|:|:|
Db      1 DPIGHL 6

RESULT 39
US-10-149-135-1487
; Sequence 1487, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Betteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1487
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1487

Query Match      72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 XXVXHL 8
       :|:|:|
Db      2 VPISHL 7

RESULT 40
US-10-149-135-1651
; Sequence 1651, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Betteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1651

Query Match      72.0%; Score 18; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 XXVXHL 8
       :|:|:|
Db      2 DPIGHL 7

RESULT 41
US-10-149-135-1763
; Sequence 1763, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Betteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1763
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; PRIOR APPLICATION NUMBER: US 08/073,205  
 ; PRIOR FILING DATE: 1993-06-04  
 ; PRIOR APPLICATION NUMBER: US 08/027,146  
 ; PRIOR FILING DATE: 1993-03-05  
 ; NUMBER OF SEQ ID NOS: 2479  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1763  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Artificial Peptide  
 US-10-149-135-1763

Query Match 72.0%; Score 18; DB 12; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8  
 DB 2 VPISHL 7

RESULT 42  
 US-10-149-135-1854  
 ; Sequence 1854, Application US/10149135  
 ; Publication No. US20040053822A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fike, John  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Sidney, John  
 ; APPLICANT: Southwood, Scott  
 ; APPLICANT: Chesnut, Robert  
 ; APPLICANT: Celis, Esteban  
 ; APPLICANT: Keogh, Elissa  
 ; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
 ; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions  
 ; FILE REFERENCE: 2060.0130001  
 ; CURRENT FILING DATE: 2000-12-11  
 ; PRIOR APPLICATION NUMBER: PCT/US00/33545  
 ; PRIOR FILING DATE: 2000-12-11  
 ; PRIOR APPLICATION NUMBER: US 09/458,298  
 ; PRIOR FILING DATE: 1999-12-10  
 ; PRIOR APPLICATION NUMBER: US 09/189,702  
 ; PRIOR FILING DATE: 1998-11-10  
 ; PRIOR APPLICATION NUMBER: US 08/205,713  
 ; PRIOR FILING DATE: 1994-03-04  
 ; PRIOR APPLICATION NUMBER: US 08/159,184  
 ; PRIOR FILING DATE: 1993-11-29  
 ; PRIOR APPLICATION NUMBER: US 08/073,205  
 ; PRIOR FILING DATE: 1993-06-04  
 ; PRIOR APPLICATION NUMBER: US 08/027,146  
 ; PRIOR FILING DATE: 1993-03-05  
 ; NUMBER OF SEQ ID NOS: 2479  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1854  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Artificial Peptide  
 US-10-149-135-1854

Query Match 72.0%; Score 18; DB 12; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8  
 DB 2 DPIGHL 7

RESULT 43  
 US-10-149-135-2451  
 ; Sequence 2451, Application US/10149135  
 ; Publication No. US20040053822A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fike, John  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Sidney, John  
 ; APPLICANT: Southwood, Scott  
 ; APPLICANT: Chesnut, Robert  
 ; APPLICANT: Celis, Esteban  
 ; APPLICANT: Keogh, Elissa  
 ; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
 ; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions  
 ; FILE REFERENCE: 2060.0130001  
 ; CURRENT FILING DATE: 2000-12-11  
 ; PRIOR APPLICATION NUMBER: PCT/US00/33545  
 ; PRIOR FILING DATE: 2000-12-11  
 ; PRIOR APPLICATION NUMBER: US 09/458,298  
 ; PRIOR FILING DATE: 1999-12-10  
 ; PRIOR APPLICATION NUMBER: US 09/189,702  
 ; PRIOR FILING DATE: 1998-11-10  
 ; PRIOR APPLICATION NUMBER: US 08/205,713  
 ; PRIOR FILING DATE: 1994-03-04  
 ; PRIOR APPLICATION NUMBER: US 08/159,184  
 ; PRIOR FILING DATE: 1993-11-29  
 ; PRIOR APPLICATION NUMBER: US 08/073,205  
 ; PRIOR FILING DATE: 1993-06-04  
 ; PRIOR APPLICATION NUMBER: US 08/027,146  
 ; PRIOR FILING DATE: 1993-03-05  
 ; NUMBER OF SEQ ID NOS: 2479  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2451  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Artificial Peptide  
 US-10-149-135-2451

Query Match 72.0%; Score 18; DB 12; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8  
 DB 1 PPISHL 6

RESULT 44  
 US-10-387-957-6  
 ; Sequence 6, Application US/10387957  
 ; Publication No. US20040052809A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Glaxosmithkline Biologicals s.a.  
 ; TITLE OF INVENTION: Vaccine  
 ; FILE REFERENCE: B45284  
 ; CURRENT FILING DATE: 2003-03-13  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 6  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-387-957-6

Query Match 72.0%; Score 18; DB 12; Length 8;  
 Best Local Similarity 28.6%; Pred. No. 1.2e+06;  
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7

Db 1 MCGYMKH 7

RESULT 45  
 US-10-632-388-537  
 ; Sequence 537, Application US/10632388  
 ; Publication No. US20040053845A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FEIGE, ULRICH  
 ; APPLICANT: LIU, CHUAN-PA  
 ; APPLICANT: CHEETHAM, JANET C.  
 ; APPLICANT: BOONE, THOMAS CHARLES  
 ; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
 ; FILE REFERENCE: A-527  
 ; CURRENT APPLICATION NUMBER: US/10/632,388  
 ; CURRENT FILING DATE: 2003-07-31  
 ; PRIOR APPLICATION NUMBER: US/09/428,082B  
 ; PRIOR FILING DATE: 1999-10-22  
 ; PRIOR APPLICATION NUMBER: 60/105,371  
 ; PRIOR FILING DATE: 1998-10-23  
 ; NUMBER OF SEQ ID NOS: 113  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 537  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: ANTIPATHOGENIC PEPTIDE  
 US-10-632-388-537

Query Match 72.0%; Score 18; DB 12; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 1.2e+06;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 XVXHL 8  
 :|||  
 Db 1 KVFHL 5

Search completed: August 19, 2004, 16:00:18  
 Job time : 38 secs

*This Page Blank (uspto)*



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: August 19, 2004, 15:47:57 ; Search time 11.5 Seconds  
(without alignments)  
66.916 Million cell updates/sec

Title: VARIANT1  
Perfect score: 25  
Sequence: 1 XQXXVXHL 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 148

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	60.0	8	2	A61496 ubiquitin - celery
2	13	52.0	8	2	SS3008 citrate synthase -
3	12	48.0	8	2	PT0368 Ig gamma chain C r
4	11	44.0	8	2	A31570 angiotensin-conver
5	10	40.0	8	2	T14906 hypochlorite prote
6	10	40.0	8	2	PH1618 Ig H chain V-D-J r
7	10	40.0	8	2	A42689 major postsynaptic
8	10	40.0	8	2	PC4372 telomeric and tetr
9	10	40.0	8	2	B47594 aspartate kinase (
10	9	36.0	8	2	XGHUEU urine glycopeptide
11	9	36.0	8	2	S43971 tumor-associated a
12	9	36.0	8	2	S43972 tumor-associated a
13	9	36.0	8	2	T10077 hypochlorite prote
14	9	36.0	8	2	S68802 nitrate reductase
15	9	36.0	8	2	PQ0726 unidentified 4.5/4
16	9	36.0	8	2	JS0316 leucokinin VI - Ma
17	9	36.0	8	2	PT0298 Ig heavy chain CRD
18	9	36.0	8	2	B45800 serum albumin - do
19	9	36.0	8	2	AS4823 olfactory receptor
20	9	36.0	8	2	B54823 cytochrome-c oxida
21	9	36.0	8	2	S65381 ferredoxin a2 - Ja
22	9	36.0	8	2	S69165 L-serine ammonia-1
23	9	36.0	8	2	A25836 neuopeptide B - b
24	8	32.0	8	2	B24749 acylase - Kluyvera
25	8	32.0	8	2	S19288 1pgf protein - Shi
26	8	32.0	8	2	S70727 dissimilatory sulf
27	8	32.0	8	2	S63493 protein QA300039 -
28	8	32.0	8	2	PA0035 hypochlorite prote
29	8	32.0	8	2	T10952

30	8	32.0	8	2	S78036 ribosomal protein
31	8	32.0	8	2	PT0030 inulinase (EC 3.2.
32	8	32.0	8	2	PT0162 paramyosin - north
33	8	32.0	8	2	A46306 spasmogenic toxin
34	8	32.0	8	2	A14683 aspartate transami
35	8	32.0	8	2	PT0323 Ig heavy chain CRD
36	8	32.0	8	2	PN0043 phosphatidylethano
37	8	32.0	8	2	I49404 prealbumin - weste
38	8	32.0	8	2	C39690 neutral cell adhesi
39	8	32.0	8	2	A35180 neutral proteinase
40	8	32.0	8	2	S29272 tocopherol-binding
41	7	28.0	8	2	A61348 red pigment-concen
42	7	28.0	8	2	A28004 adipokinetic hormo
43	7	28.0	8	2	S08995 hypertrehalosemic
44	7	28.0	8	2	S08996 hypertrehalosemic
45	7	28.0	8	2	S10596 adipokinetic hormo

## ALIGNMENTS

RESULT 1  
A61496  
ubiquitin - celery (fragment)  
C:Species: Apium graveolens (celery)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 07-May-1999  
C:Accession: A61496  
R:Goldstein, G.; Scheid, M.; Hammerling, U.; Boyse, E.A.; Schlessinger, D.H.; Niall, H.D.  
Proc. Natl. Acad. Sci. U.S.A. 72, 11-15, 1975  
A:Title: Isolation of a polypeptide that has lymphocyte-differentiating properties and is  
A:Reference number: A61496; PMID:75120426; PMID:1078892  
A:Accession: A61496  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <GOL>  
A>Note: a small amount of material was sequenced; the amino-terminal residue is unlikely

Query Match  
Best Local Similarity 60.0%; Score 15; DB 2; Length 8;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XQXXVXHL 8  
Db 1 XQIXVKTL 8

RESULT 2  
S53008  
citrate synthase - cucurbit  
C:Species: Cucurbita sp. (cucurbit)  
C:Date: 14-Jul-1995 #sequence\_revision 03-Nov-1995 #text\_change 17-Mar-1999  
C:Accession: S53008  
R:Kato, A.; Hayashi, M.; Mori, H.; Nishimura, M.  
Plant Mol. Biol. 27, 377-390, 1995  
A:Title: Molecular characterization of a glyoxysomal citrate synthase that is synthesized  
A:Reference number: S53007; PMID:95195164; PMID:7888626  
A:Accession: S53008  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <KAT>

Query Match  
Best Local Similarity 52.0%; Score 13; DB 2; Length 8;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XQXXVX 6  
Db 2 AQTMVA 7

RESULT 3  
PT0368  
Ig gamma chain C region (gamma-1) - human (fragment)

C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Aug-1996  
 C:Accession: P0368  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C:Accession: P0368  
 A:Title: Early occurrence of immunoglobulin isotype switching in human fetal liver.  
 A:Reference number: P0368; PMID:91312348; PMID:1506981  
 A:Accession: P0368  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <ML>  
 A:Experimental source: fetal liver  
 C:Keywords: immunoglobulin

Query Match 48.0%; Score 12; DB 2; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXV 6  
 :|:|:  
 Db 2 HQGPIG 7

## RESULT 4

A31570  
 angiotensin-converting enzyme inhibitor - yellowfin tuna  
 C:Species: Thunnus albacares (yellowfin tuna)  
 C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 18-Aug-2000  
 C:Accession: A31570  
 R:Kohma, Y.; Matsunoto, S.; Oka, H.; Terramoto, T.; Okabe, M.; Mimura, T.  
 Biochem. Biophys. Res. Commun. 155, 332-337, 1988  
 A:Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.  
 A:Reference number: A31570; PMID:88326322; PMID:3415688  
 A:Accession: A31570  
 A:Molecule type: protein  
 A:Residues: 1-8 <KH>  
 A:Note: the source is designated as Neothunnus macropterus  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 44.0%; Score 11; DB 2; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHL 8  
 :|:  
 Db 2 TH1 4

## RESULT 5

T14906  
 hypothetical protein - parsley  
 C:Species: Petroselinum crispum (parsley)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T14906  
 R:Feldbrugge, M.; Sprenger, M.; Dinkelbach, M.; Yazaki, K.; Harter, K.; Weisshaar, B.  
 Plant Cell 6, 1607-1621, 1994  
 A:Title: Functional analysis of a light-responsive plant bZIP transcriptional regulator.  
 A:Reference number: T14906; PMID:95128172; PMID:7827494  
 A:Accession: T14906  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <FL>  
 A:Cross-references: EMBL:575395; NID:9913201; PID:el94245

Query Match 40.0%; Score 10; DB 2; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VXH 7  
 :|:|:  
 Db 1 MKH 3

## RESULT 6

PH618  
 Ig H chain V-D-J region (clone B-1ees 33) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C:Accession: PH618  
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-1ees mice  
 A:Reference number: PH618; PMID:93301609; PMID:8315387  
 A:Accession: PH618  
 A:Molecule type: DNA  
 A:Residues: 1-8 <LE>  
 A:Experimental source: bone marrow pre-B lymphocyte  
 C:Keywords: immunoglobulin

Query Match 40.0%; Score 10; DB 2; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 XVXH 7  
 :|:|:  
 Db 1 CARH 4

## RESULT 7

A42689  
 major postsynaptic density protein - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 26-May-1994  
 C:Accession: A42689  
 R:Wu, K.; Huang, Y.; Adler, J.; Black, I.B.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 3015-3019, 1992  
 A:Title: On the identity of the major postsynaptic density protein.  
 A:Reference number: A42689; PMID:92212358; PMID:1313576  
 A:Accession: A42689  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <WNA>

Query Match 40.0%; Score 10; DB 2; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8  
 :|:|:|:  
 Db 2 LKVPNT 7

## RESULT 8

PC4372  
 telomeric and tetraplex DNA binding protein qTBP42 II - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Oct-1997 #sequence\_revision 28-Oct-1997 #text\_change 07-May-1999  
 C:Accession: PC4372  
 R:Barry, G.; Weisman-Shomer, P.; Fry, M.  
 Biochem. Biophys. Res. Commun. 237, 617-623, 1997  
 A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CAI  
 A:Reference number: PC4372; PMID:97445086; PMID:9299414  
 A:Accession: PC4372  
 A:Molecule type: protein  
 A:Residues: 1-8 <SAR>  
 A:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular  
 F/3-8/Domain: RNP2 #status predicted <RNP>

Query Match 40.0%; Score 10; DB 2; Length 8;  
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 OXXVXHL 8  
 :|:|:|:  
 Db 1 KXFGGL 7

## RESULT 9

B47594

aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain N13) (fragment)

C/Species: Corynebacterium flavum  
C/Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 19-Dec-1997  
C/Accession: B47594

R/Pollett, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinskey, A.J.

J. Bacteriol. 175, 4096-4103, 1993

A/Title: Gene structure and expression of the Corynebacterium flavum N13 ask-*asd* operon.

A/Reference number: A47594; MUID:93308089; PMID:8100567

A/Status: preliminary; not compared with conceptual translation

A/Accession: B47594

A/Molecule type: DNA

A/Residues: 1-8 &lt;FOL&gt;

C/Keywords: phosphotransferase

Query Match

Best Local Similarity 40.0%; Score 10; DB 2; Length 8;

Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 XQXXV 6

DB 1 MEEAVL 6

## RESULT 10

XGHUEU

urine glycopeptide - human

C/Species: Homo sapiens (man)

C/Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C/Accession: A03188

R/Lote, C.J.; Weiser, J.B.

Biochem. J. 123, 25P, 1971

A/Title: Identification in urine of a low-molecular-weight polar glycopeptide containing

A/Reference number: A03188; MUID:72062338; PMID:5126885

A/Accession: A03188

A/Molecule type: protein

A/Residues: 1-8 &lt;LOT&gt;

C/Comment: The identity of the glycoprotein from which this peptide is derived is unknown

C/Superfamily: unassigned animal peptides

C/Keywords: glycoprotein

F/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match

Best Local Similarity 36.0%; Score 9; DB 2; Length 8;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 XH 7

DB 2 EH 3

Query Match

Best Local Similarity 36.0%; Score 9; DB 2; Length 8;

Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 XQXXV 6

DB 2 EQWTAQ 7

## RESULT 12

S43972

tumor-associated antigen MUT2 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 20-Oct-1994 #sequence\_revision 17-Nov-1995 #text\_change 18-Aug-2000  
C/Accession: S43972

R/Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.

Nature 369, 67-71, 1994

A/Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine

A/Reference number: S43971; MUID:94217811; PMID:8164742

A/Accession: S43972

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-8 &lt;MAN&gt;

C/Superfamily: unassigned animal peptides

## RESULT 13

T10077

hypothetical protein N - Methylophilus methylotrophus (fragment)

C/Species: Methylophilus methylotrophus

C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C/Accession: T10077

R/Chistoserdov, A.Y.; McIntire, W.S.; Mathews, F.S.; Lidstrom, M.E.

J. Bacteriol. 176, 4073-4080, 1994

A/Title: Organization of the methyline utilization (*mau*) genes in *Methylophilus methyl-*

A/Reference number: Z16936; MUID:94292427; PMID:8021188

A/Accession: T10077

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-8 &lt;CHT&gt;

A/Cross-references: EMBL:126407; NID:9561931; PIDN:AMB4655.1; PID:9561933

A/Experimental source: strain W3A1

A/Genes: mauN

Query Match

Best Local Similarity 36.0%; Score 9; DB 2; Length 8;

Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 XQXXV 5

DB 4 LQAIL 8

Query Match

Best Local Similarity 36.0%; Score 9; DB 2; Length 8;

Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

## RESULT 14

S68802

nitrate reductase (NADH) inhibitor - spinach (fragment)

C/Species: Spinacia oleracea (spinach)

C/Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998  
C/Accession: S68802

R/Bachmann, M.; Huber, J.L.; Liao, P.C.; Gage, D.A.; Huber, S.C.

FEBS Lett. 387, 127-131, 1996

A/Title: The inhibitor protein of phosphorylated nitrate reductase from spinach (*Spinacia*

A/Reference number: S68802; MUID:96244508; PMID:8674533

A/Accession: S68802

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-8 &lt;BAC&gt;

A/Experimental source: leaves; strain cv. Bloomsdale

Query Match 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 20.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 XXVXH 7  
 :|::|  
 Db 3 LSVAY 7

RESULT 15  
 P00726  
 unidentified 4.5/45K [imported] - rice (fragment)  
 C/Species: Oryza sativa (rice)  
 C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C/Accession: P00726  
 R/Komatsu, S.; Kajiwara, H.; Hirano, H.  
 Theor. Appl. Genet. 86, 935-942, 1993  
 A/Title: A rice protein library; a data-file of rice proteins separated by two-dimension  
 A/Reference number: P00696  
 A/Accession: P00726  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-8 <KOM>

Query Match 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 X0XXVX 6  
 :|::|  
 Db 2 V00DAA 7

RESULT 16  
 J50316  
 leucokinin VI - Madeira cockroach  
 C/Species: Leucophaea maderae (Madeira cockroach)  
 C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C/Accession: J50316  
 R/Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 27-30, 1987  
 A/Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotropic  
 A/Reference number: J50315  
 A/Accession: J50316  
 A/Molecule type: protein  
 A/Residues: 1-8 <HO>  
 C/Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act  
 C/Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid  
 F1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
 F1/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7  
 :|  
 Db 4 FH 5

RESULT 17  
 P70298  
 Ig heavy chain CRD3 region (clone 5-103A) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C/Accession: P70298  
 R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
 A/Reference number: P70222; MWID:91108337; PMID:1899102  
 A/Accession: P70298  
 A/Molecule type: DNA

A/Residues: 1-8 <YAM>  
 A/Experimental source: B lymphocyte  
 C/Keywords: heterotrimer; immunoglobulin  
 Query Match 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 28.6%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 QXXVXHL 8  
 :|::|  
 Db 1 RMTVVVL 7

RESULT 18  
 B45800  
 serum albumin - dog (fragment)  
 C/Species: Canis lupus familiaris (dog)  
 C/Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 31-Dec-1993  
 C/Accession: B45800  
 R/Carraway, R.E.; Cochran, D.E.; Boucher, W.; Mitra, S.P.  
 J. Immunol. 143, 1680-1684, 1989  
 A/Title: Structures of histamine-releasing peptides formed by the action of acid protease  
 A/Reference number: A45800; MWID:89341406; PMID:2474609  
 A/Accession: B45800  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-8 <CAR>

Query Match 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7  
 :|  
 Db 4 RH 5

RESULT 19  
 A54823  
 olfactory receptor I7 - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 17-Mar-1999  
 C/Accession: A54823  
 R/Chess, A.; Simon, I.; Cedar, H.; Axel, R.  
 Cell 78, 823-834, 1994  
 A/Title: Allelic inactivation regulates olfactory receptor gene expression.  
 A/Reference number: A54823; MWID:94373818; PMID:8087849  
 A/Accession: A54823  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-8 <CHE>

Query Match 36.0%; Score 9; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7  
 :|  
 Db 5 NH 6

RESULT 20  
 B54823  
 olfactory receptor I7 - western wild mouse (fragment)  
 C/Species: Mus spretus (western wild mouse)  
 C/Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 17-Mar-1999  
 C/Accession: B54823  
 R/Chess, A.; Simon, I.; Cedar, H.; Axel, R.  
 Cell 78, 823-834, 1994  
 A/Title: Allelic inactivation regulates olfactory receptor gene expression.  
 A/Reference number: A54823; MWID:94373818; PMID:8087849  
 A/Accession: B54823  
 A/Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-8 <CHE>

Query Match 36.0%; Score 9; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7  
DB 5 NH 6

## RESULT 21

S65381

Cytochrome-c oxidase (EC 1.9.3.1) chain VIIb, hepatic - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999

C/Accession: S65381

R/Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995

A/Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term

A/Reference number: S65372; MUID:95324523; PMID:7601105

A/Accession: S65381

A/Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <SCH>

C/Keywords: oxidoreductase

Query Match 36.0%; Score 9; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXVX 6  
DB 1 QNXLD 5

## RESULT 22

S69165

Ferredoxin a2 - Japanese radish (fragment)

C/Species: Kaiware daikon (Japanese radish)

C/Date: 10-Mar-1998 #sequence\_revision 10-Mar-1998 #text\_change 17-Apr-1998

C/Accession: S69165

R/Obara, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.

Arch. Biochem. Biophys. 316, 797-802, 1995

A/Title: Four ferredoxins from Japanese radish leaves.

A/Reference number: S69164; MUID:95168867; PMID:7864635

A/Accession: S69165

A:Molecule type: protein

A:Residues: 1-8 <OBA>

C/Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 36.0%; Score 9; DB 2; Length 8;  
Best Local Similarity 20.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXV 5  
DB 4 EBDIV 8

## RESULT 23

A25836

L-serine ammonia-lyase (EC 4.3.1.17) - Escherichia coli (fragment)

C/Species: Escherichia coli

C/Date: 24-Jan-1988 #sequence\_revision 24-Jan-1988 #text\_change 21-Jun-2002

C/Accession: A25836

R/Heinze, M.C.; McFall, E.

J. Bacteriol. 123, 1163-1168, 1975

A/Title: N-terminal amino acid sequences of D-serine deaminases of wild-type and operat

A/Reference number: A25836; MUID:76005414; PMID:1099073

A/Contents: K12

A/Accession: A25836

A:Molecule type: protein  
A:Residues: 1-8 <HEI>  
C/Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; seri

Query Match 36.0%; Score 9; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XH 7  
DB 6 RH 7

## RESULT 24

B24749

neuropeptide B - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Aug-2000

C/Accession: B24749

R/Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.

Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985

A/Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b

A/Reference number: A94074; MUID:86067985; PMID:3865193

A/Accession: B24749

A:Molecule type: protein

A:Residues: 1-8 <YAN>

C/Superfamily: unassigned animal peptides

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
DB 3 FQPO 6

## RESULT 25

S19288

acylase - Kluyvera cryocrescens

C/Species: Kluyvera cryocrescens

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C/Accession: S19288

R/Martin, J.; Slade, A.; Altken, A.; Arche, R.; Virden, R.

Biochem. J. 280, 659-662, 1991

A/Title: Chemical modification of serine at the active site of penicillin acylase from K

A/Reference number: S19288; MUID:92109664; PMID:1764029

A/Accession: S19288

A/Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <MAR>

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXVX 6  
DB 1 CNMVI 6

## RESULT 26

S70727

lgpF protein - Shigella flexneri (fragment)

C/Species: Shigella flexneri

C/Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 08-Oct-1999

C/Accession: S70727

R/Alaoui, A.; Sansonetti, P.J.; Menard, R.; Barzu, S.; Mounier, J.; Phalipon, A.; Parot

Mol. Microbiol. 17, 461-470, 1995

A/Title: Mxlg, a membrane protein required for secretion of Shigella spp. Tpa invasins: 1

A/Reference number: S70727; MUID:96100445; PMID:8559065

A/Accession: S70727

A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-8 <ALT>  
A:Cross-references: EMBL:248957; NID:92929880; PID:CAA8821.1; PID:92929881  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995  
C:Genetics:  
A:Gene: 199F

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
:|:|:  
DB 2 KQNN 5

## RESULT 27

S63493  
disimilatory sulfite reductase gamma chain, membrane-bound and soluble - Desulfovibrio  
C:Species: Desulfovibrio desulfuricans  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
C:Accession: S63493; S63494  
R:Steuber, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.  
Eur. J. Biochem. 233, 873-879, 1995  
A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio  
A:Reference number: S63489; MUID:96085152; PMID:8521853  
A:Accession: S63493  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <STE>  
A:Accession: S63494  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <ST2>

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 0.0%; Pred. No. 2.8e+05;  
Matches 0; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7  
:|:|:|:  
DB 1 AEITY 5

## RESULT 28

PA0035  
protein QA300039 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C:Accession: PA0035  
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
Submitted to JPIPI, July 1994  
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensions  
A:Reference number: PA0001  
A:Accession: PA0035  
A:Molecule type: protein  
A:Residues: 1-8 <KAM>  
A:Experimental source: stem

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
:|:|:|:  
DB 1 LQXD 4

## RESULT 29

T10952  
hypothetical protein 1 - spring vetch  
C:Species: Vicia sativa (spring vetch, tare)

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: T10952  
R:Christiansen, A.; Hansen, A.C.; Viijn, I.; Pallisgaard, N.; Larsen, K.; Yang, W.C.; Bisse  
submitted to the EMBL Data Library, December 1995  
A:Description: A novel type of DNA binding protein interacts with a conserved sequence in  
A:Reference number: Z17228

A:Accession: T10952  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-8 <CHR>  
A:Cross-references: EMBL:X95995; NID:g1360633; PID:e225824

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVX 6  
:|:|:|:  
DB 2 MMTLVS 7

## RESULT 30

S78036  
ribosomal protein Yms-B, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)  
C:Species: Saccharomyces cerevisiae  
C:Date: 09-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 14-Nov-1997  
C:Accession: S78036  
R:Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldechmidt-Reisin, S.; Herfurth, E.; Wittmar  
Eur. J. Biochem. 245, 449-456, 1997  
A:Title: Identification and characterization of the genes for mitochondrial ribosomal pr  
A:Reference number: S78018; MUID:97296414; PMID:9151578  
A:Accession: S78036  
A:Molecule type: protein  
A:Residues: 1-8 <KIT>  
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVX 6  
:|:|:|:  
DB 1 MNXXVD 6

## RESULT 31

PT0030  
inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)  
N:Alternate names: inulase  
C:Species: Aspergillus ficuum  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 07-May-1999  
C:Accession: PT0030  
R:Eltalibi, M.; Baratt, J.C.  
Agric. Biol. Chem. 54, 61-68, 1990  
A:Title: Molecular and kinetic properties of Aspergillus ficuum inulinases.  
A:Reference number: PT0030; MUID:90344234; PMID:1368526  
A:Accession: PT0030  
A:Molecule type: protein  
A:Residues: 1-8 <ETP>  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
:|:|:|:  
DB 4 DQPY 7

## RESULT 32

PL0162  
paramyosin - northern quahog (fragment)

C:/Species: Mercenaria mercenaria (northern quahog)  
C:/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 11-May-2000  
C:/Accession: P10162  
R/Matabe, S.; Teuchiya, T.; Hartshorne, D.J.  
Comp. Biochem. Physiol. B 94, 813-821, 1989  
A:/Title: Phosphorylation of paramyosin.  
A:/Reference number: P10162; MUID:90107385; PMID:2532591  
C:/Accession: P10162  
A:/Molecule type: protein  
A:/Residues: 1-8 <MAT>  
A:/Experimental source: white adductor muscle  
A:/Note: The sequence is the phosphorylated tryptic peptide  
C:/Comment: This protein is thought to exist as a dimer of two subunits, termed alpha-par  
om the carboxyl-terminal end of the molecule. Only alpha-paramyosin is phosphorylated by  
C:/Keywords: muscle; phosphoprotein  
P/5/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXX 6  
: : :  
Db 2 RMSVS 7

RESULT 33  
A46306  
spasmogenic toxin PNVI - spider (Phoneutria nigricincta) (fragment)  
C:/Species: Phoneutria nigricincta  
C:/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 17-Mar-1999  
C:/Accession: A46306  
R/Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.  
Toxicol. 31, 377-384, 1993  
A:/Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide  
A:/Reference number: A46306; MUID:93276438; PMID:8503129  
C:/Accession: A46306  
A:/Status: preliminary  
A:/Molecule type: protein  
A:/Residues: 1-8 <MAR>

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
: : :  
Db 5 GOST 8

RESULT 34  
A14683  
aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragm  
N:/Alternate names: aspartate aminotransferase, mitochondrial  
C:/Species: Gallus gallus (chicken)  
C:/Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000  
C:/Accession: A14683  
R/Wilson, K.V.; Hunziker, P.; Hughes, G.J.  
FEBS Lett. 108, 98-102, 1979  
A:/Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.  
A:/Reference number: A14683; MUID:80092116; PMID:520566  
C:/Accession: A14683  
A:/Molecule type: protein  
A:/Residues: 1-8 <WIL>  
C:/Keywords: aminotransferase; mitochondrion

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
: : :  
Db 5 GOST 8

RESULT 35  
PT0323  
Ig heavy chain C/D3 region (clone J2-106B) - human (fragment)  
C:/Species: Homo sapiens (man)  
C:/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:/Accession: PT0323  
R/Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jc  
A:/Reference number: PT0323; MUID:9108337; PMID:1899102  
C:/Accession: PT0323  
A:/Molecule type: DNA  
A:/Residues: 1-8 <YAM>  
A:/Experimental source: B lymphocyte  
C:/Keywords: heterotetramer; immunoglobulin

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
: : :  
Db 4 GOST 7

RESULT 36  
PN0043  
phosphatidylethanol amine-binding protein - mouse (fragment)  
C:/Species: Mus musculus (house mouse)  
C:/Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998  
C:/Accession: PN0043  
R/Kato, H.  
Kawasaki Igakashi 22, 245-259, 1996  
A:/Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neurot  
A:/Reference number: PN0041  
C:/Accession: PN0043  
A:/Molecule type: protein  
A:/Residues: 1-8 <KAT>  
A:/Experimental source: neuroblastoma cell  
C:/Comment: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is blocked.  
C:/Keywords: brain

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXX 4  
: : :  
Db 3 EQLS 6

RESULT 37  
I49404  
prealbumin - western wild mouse (fragment)  
C:/Species: Mus spretus (western wild mouse)  
C:/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:/Accession: I49404  
R/Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.  
Mamm. Genome 5, 349-355, 1994  
A:/Title: Genetic mapping of 40 cDNA clones from the mouse genome by PCR.  
A:/Reference number: I49404; MUID:94319082; PMID:8043949  
C:/Accession: I49404  
A:/Molecule type: protein  
A:/Status: preliminary; translated from GB/EMBL/DBJ  
A:/Residues: 1-8 <RES>  
A:/Cross-references: EMBL:U05689; NID:9497008; PIDN:AA60461.1; PID:9642825

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 20.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVXH 7  
:|:|:  
Db 1 AVVSN 5

## RESULT 38

A35180  
C39690  
neural cell adhesion molecule, cardiac splice form '-', '-' - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
C/Accession: C39690  
R/Reyes, A.A.; Small, S.J.; Akesson, R.  
Mol. Cell. Biol. 11, 1654-1661, 1991  
A/Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mR  
A/Reference number: A39690; MUID:91141516; PMID:1996115  
A/Accession: C39690  
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A/Molecule type: mRNA  
A/Residues: 1-8 <REY>  
A/Cross-references: GB:M63970  
C/Keywords: cardiac muscle; cell adhesion; heart

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 XQXX 4  
:|:|:  
Db 3 VQGE 6

## RESULT 39

A35180  
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 21-Mar-1996  
C/Accession: A35180  
R/Toshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Satoh, M.  
J. Biol. Chem. 265, 5809-5815, 1990  
A/Title: Purification of a novel type of calcium-activated neutral protease from rat bra  
A/Reference number: A35180; MUID:90202830; PMID:2318836  
A/Accession: A35180  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-8 <YOS>  
C/Keywords: hydrolase

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 16.7%; Pred. No. 2.8e+05;  
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 XQXXVX 6  
:|:|:  
Db 3 LSEGVP 8

## RESULT 40

S29272  
tocoopherol-binding protein. 81K - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 22-Nov-1993 #sequence\_revision 12-Apr-1996 #text\_change 12-Apr-1996  
C/Accession: S29272  
R/Nalecz, K.A.; Nalecz, M.J.; Azzi, A.  
Eur. J. Biochem. 209, 37-42, 1992  
A/Title: Isolation of tocoopherol-binding proteins from the cytosol of smooth muscle A7r5  
A/Reference number: S29272; MUID:93011150; PMID:1396710  
A/Accession: S29272  
A/Molecule type: protein  
A/Residues: 1-8 <NAL>  
A/Experimental source: smooth muscle A7r5 cells

Query Match 32.0%; Score 8; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 XQXX 4  
:|:|:  
Db 4 DQXQ 7

## RESULT 41

A61348  
red pigment-concentrating hormone - northern shrimp  
N/Alternate names: blanching hormone  
C/Species: Pandalus borealis (northern shrimp)  
C/Date: 02-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C/Accession: A61348; S07139  
R/Fernlund, P.; Josefsson, L.  
Science 177, 173-175, 1972  
A/Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.  
A/Reference number: A61348; MUID:72228738; PMID:5041363  
A/Accession: A61348  
A/Molecule type: protein  
A/Residues: 1-8 <FER1>  
R/Fernlund, P.

Biochim. Biophys. Acta 371, 304-311, 1974  
A/Title: Structure of the red pigment-concentrating hormone of the shrimp, Pandalus bore  
A/Reference number: S07139; MUID:75054965; PMID:4433569  
A/Accession: S07139  
A/Molecule type: protein  
A/Residues: 'E', 2-8 <FER2>

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C/Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pic  
zed pigment-containing cells.

C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/6/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.0%; Score 7; DB 2; Length 8;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QXX 4  
:|:|:  
Db 1 QLN 3

## RESULT 42

A28004  
adipokinetic hormone G - two-spotted cricket  
N/Alternate names: AKH-G  
C/Species: Gryllus bimaculatus (two-spotted cricket)  
C/Date: 30-Jun-1989 #sequence\_revision 24-Oct-1997 #text\_change 24-Oct-1997  
C/Accession: A28004  
R/Gade, G.; Rinehart, K.L.  
Biochem. Biophys. Res. Commun. 149, 908-914, 1987  
A/Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptic  
A/Reference number: A28004; MUID:88106553; PMID:3426616  
A/Accession: A28004  
A/Molecule type: protein  
A/Residues: 1-8 <GAB>  
A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/6/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.0%; Score 7; DB 2; Length 8;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QXX 4  
:|:|:  
Db 1 QVN 3



## RESULT 43

S08995 hypertrehalosemic hormone I - oriental cockroach

N/Alternate names: Pea-CAH-I

C/Species: Blatta orientalis (oriental cockroach)

C/Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997

C/Accession: S08995

R/Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Ectatosoma tiaratum assigned by tandem fast atom bombard

A/Reference number: S08995; PMID:2340112

A/Accession: S08995

A/Molecule type: protein

A/Residues: 1-8 &lt;GAE&gt;

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 28.0%; Score 7; DB 2; Length 8;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

DB 1 QVN 3

RESULT 44

S08996 hypertrehalosemic hormone II - oriental cockroach

N/Alternate names: Pea-CAH-II

C/Species: Blatta orientalis (oriental cockroach)

C/Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997

C/Accession: S08996

R/Gaede, G.; Rinehart, K.L.

Biol. Chem. Hoppe-Seyler 371, 345-354, 1990

A/Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Ectatosoma tiaratum assigned by tandem fast atom bombard

A/Reference number: S08995; PMID:2340112

A/Accession: S08996

A/Molecule type: protein

A/Residues: 1-8 &lt;GAE&gt;

A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 28.0%; Score 7; DB 2; Length 8;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

DB 1 QVN 3

RESULT 45

S10596 adipokinetic hormone - pond skimmer

C/Species: Libellula auripennis

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 14-Nov-1997

C/Accession: S10596

R/Gaede, G.

Biol. Chem. Hoppe-Seyler 371, 475-483, 1990

A/Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating ho

A/Reference number: S10596; PMID:2390213

A/Accession: S10596

A/Molecule type: protein

A/Residues: 1-8 &lt;BIO&gt;

C/Comment: This peptide has both adipokinetic and hypertrehalosemic activities.

C/Superfamily: adipokinetic hormone

C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 28.0%; Score 7; DB 2; Length 8;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

DB 1 QVN 3

Search completed: August 19, 2004, 15:51:22

Job time : 12.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 19, 2004, 15:47:57 ; Search time 8 Seconds

(Without alignments)  
52.070 Million cell updates/sec

Title: VARIANT1

Perfect score: 25

Sequence: 1 XQXXVXHL 8

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 8

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	48.0	8	1 FUSO	PE1010 fusarium so
2	11	44.0	8	1 ACI_THUAL	PE18691 thunnus alb
3	10	40.0	8	1 ANG2_BORJA	Q10582 bochrups ja
4	10	40.0	8	1 CPD1_ENTFA	P13269 enterococcu
5	10	40.0	8	1 UPAL_HUMAN	P30087 homo sapien
6	9	36.0	8	1 ALI1_CYPPO	PE2152 cydia pomon
7	9	36.0	8	1 COXG_RAT	PE0430 rattus norv
8	9	36.0	8	1 GLUR_HUMAN	P02729 homo sapien
9	9	36.0	8	1 LCK4_LEUMA	P11143 leucophaea
10	9	36.0	8	1 LCK6_LEUMA	P19988 leucophaea
11	8	32.0	8	1 ACT_CARMA	PE0709 carcinus ma
12	8	32.0	8	1 ALI7_CARMA	PE1820 carcinus ma
13	8	32.0	8	1 B44K_PORGI	PE1886 porphyromon
14	8	32.0	8	1 CLP_THICU	PE0488 thiochacillu
15	8	32.0	8	1 LCK3_LEUMA	P11142 leucophaea
16	8	32.0	8	1 NPMB_BOVIN	P15507 bos taurus
17	8	32.0	8	1 UC26_MAIZE	PE0632 zea mays (m
18	8	32.0	8	1 UF06_MOUSE	PE8644 mus musculu
19	8	32.0	8	1 UH09_RAT	PE6575 rattus norv
20	7	28.0	8	1 AKHG_GRYBI	P4086 gryllus bim
21	7	28.0	8	1 AKH_LIBAU	P25418 libellula a
22	7	28.0	8	1 AKH_MEML	P25423 melolontha
23	7	28.0	8	1 AKH_TYBKT	P14595 tabanus atr
24	7	28.0	8	1 CAD1_ENTFA	P13268 enterococcu
25	7	28.0	8	1 COM2_CONPU	PE8785 conus purpu
26	7	28.0	8	1 FAR4_MACRS	PE3277 macrobrachi
27	7	28.0	8	1 HTP1_PERAM	PE4548 periplaneta
28	7	28.0	8	1 HTP2_PERAM	PE4549 periplaneta
29	7	28.0	8	1 HTP_TENNO	PE5419 tenebrio mo
30	7	28.0	8	1 LMT2_LOCMI	P22366 locusta mig
31	7	28.0	8	1 LPK_LEUMA	P13049 leucophaea
32	7	28.0	8	1 PUP_BRANA	PE1707 brassica na
33	7	28.0	8	1 PPK2_PERAM	PE2692 periplaneta

34	7	28.0	8	1 RPCH_PANBO	PO8939 pandanus bo
35	7	28.0	8	1 VGL6_HSV2B	PE1780 herpes simp
36	6	24.0	8	1 ALI2_CARMA	PE1815 carcinus ma
37	6	24.0	8	1 ALI7_CARMA	PE1809 carcinus ma
38	6	24.0	8	1 FAR1_PENMO	PE8316 penaeus mon
39	6	24.0	8	1 FAR2_MACRS	PE8325 macrobrachi
40	6	24.0	8	1 FAR3_HOMAM	PE1486 homarus ame
41	6	24.0	8	1 FAR4_HOMAM	PE1487 homarus ame
42	6	24.0	8	1 FAR7_ASCSU	PE43171 ascaris suu
43	6	24.0	8	1 NS3_MYCTU	PE1152 mycobacteri
44	6	24.0	8	1 PPK3_PERAM	PE2618 periplaneta
45	6	24.0	8	1 RT34_BOVIN	PE82929 bos taurus

## ALIGNMENTS

RESULT 1	FUSO	STANDARD;	PRT;	8 AA.
ID	PE1010;			
AC	PE1010;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Allergen Fus s 13596* (Fragment).			
OS	Fusarium solani (subsp. pisi) (Nectria haematococca).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.			
OX	NCBI_TaxID=70791;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN=IRI 3596; TISSUE=Mycelium;			
RA	Verma J., Gangal S.V.;			
RL	Submitted (JUL-1997) to Swiss-Prot.			
CC	-!- ALLERGEN: Causes an allergic reaction in human.			
KW	Allergen.			
FT	NON TER			
SQ	SEQUENCE 8 AA; 898 MW; C372C41F5B69041 CRC64;			
Query Match	48.0%; Score 12; DB 1; Length 8;			
Best Local Similarity	20.0%; Pred. No. 1.4e+05;			
Matches	1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;			
Qy	3 XXVXH 7			
Db	1 TIMSH 5			
RESULT 2	ACI_THUAL	STANDARD;	PRT;	8 AA.
ID	PE18691;			
AC	PE18691;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	01-NOV-1990 (Rel. 16, Last annotation update)			
DE	Angiotensin-converting enzyme inhibitor.			
OS	Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;			
OC	Scombridae; Thunnus.			
OX	NCBI_TaxID=8236;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Muscle;			
RX	MEDLINE=832632; PubMed=341568;			
RA	Kobana Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;			
RT	"Isolation of angiotensin-converting enzyme inhibitor from tuna			
RT	muscle."			
RL	Biochem. Biophys. Res. Commun. 155:332-337(1988).			
DR	PIR; A31570; A31570.			
SQ	SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;			

Query Match 44.0%; Score 11; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHXL 8  
DB 2 THH 4

## RESULT 3

ANG2\_BOTUA STANDARD; PRT; 8 AA.  
AC Q10582;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Angiotensin-like peptide II (Fragment).  
OS Bothrops jararaca (Uroaraca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Plasma;  
RX MEDLINE=96208932; PubMed=8829801;  
RA Borgersel R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
RT "Isolation and identification of angiotensin-like peptides from the  
RT plasma of the snake Bothrops jararaca."  
RL Comp. Biochem. Physiol. 113B:467-473 (1996).  
CC -1- SIMILARITY: Belongs to the serpin family.  
DR InterPro: IPR000215; Serpin.  
DR PROSITE: PS00284; SERPIN; PARTIAL.  
KM Vasocostrictor; Plasma; Serpin.  
FT NON TER 8  
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 40.0%; Score 10; DB 1; Length 8;  
Best Local Similarity 20.0%; Pred. No. 1.4e+05;  
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7  
DB 2 RYVH 6

## RESULT 4

CPD1\_ENTFA STANDARD; PRT; 8 AA.  
AC P13269;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Sex pheromone CPD1.  
OS Enterococcus faecalis (Streptococcus faecalis).  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1351;  
RN [1]  
RP SEQUENCE  
RC MEDLINE=85040388; PubMed=6436970;  
RX Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,  
RA Craig R.A., Clewell D.B.;  
RT "Isolation and structure of bacterial sex pheromone, CPD1."  
RL Science 226:849-850 (1984).  
CC -1- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
CC BACTERIOLICIN PLASMID PPDI.  
KM Pheromone.  
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 40.0%; Score 10; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 8  
DB 1 FLVHFL 6

## RESULT 5

UPAL\_HUMAN STANDARD; PRT; 8 AA.  
AC P30087;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of plasma (spot 2) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing."  
RT Electrophoresis 13:707-714 (1992).  
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 4.9, its MW is: 65 kDa.  
DR SWISS-2DPAGE; P30087; HUMAN.  
FT NON TER 1  
FT UNSURE 8  
FT NON TER 8  
SQ SEQUENCE 8 AA; 944 MW; C01772C455B806DA CRC64;

Query Match 40.0%; Score 10; DB 1; Length 8;  
Best Local Similarity 16.7%; Pred. No. 1.4e+05;  
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XOXVX 6  
DB 2 QESNV 7

## RESULT 6

ALL1\_CYPDO STANDARD; PRT; 8 AA.  
AC P82152;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydiastatin 1.  
OS Cydia pomonella (Coddling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dirysata;  
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily."  
RL Peptides 16:1301-1309 (1997).  
CC -1- SIMILARITY: Belongs to the allatostatin family.  
KM Neuropeptide; Amidation.  
FT MOD RES 8  
SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 36.0%; Score 9; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 XH 7  
:|  
Db 2 PH 3

## RESULT 7

COXG\_RAT STANDARD; PRT; 8 AA.  
ID COXG\_RAT  
AC P80430;  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome c oxidase polypeptide VIb (BC 1.9.3.1) (AED) (Fragment).  
GN COX6B.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
RP SEQUENCE.  
RC STRAIN=Wistar; TISSUE=Liver;  
RX MEDLINE=95324529; PubMed=7601105;  
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;  
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and  
RT amino-terminal sequences suggest identity of the fetal heart and the  
adult liver isoform."  
RL Eur. J. Biochem. 230:235-241(1995).  
CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide  
CC chains of cytochrome c oxidase, the terminal oxidase in  
CC mitochondrial electron transport. This protein may be one of the  
CC heme-binding subunits of the oxidase.  
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase VIb family.  
DR PIR; S65381; S65381.  
KW Oxidoreductase; Mitochondrion.  
FT NON TER 1  
FT NON TER 8  
SQ SEQUENCE 8 AA, 1039 MW, 8101E9CAA73AE456 CRC64;  
Query Match 36.0%; Score 9; DB 1; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 QXXVX 6  
:|:  
Db 1 QNXLD 5

## RESULT 8

GLUR\_HUMAN STANDARD; PRT; 8 AA.  
ID GLUR\_HUMAN  
AC P02729;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Urine glycopeptide.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI\_TaxID=9606;  
RP SEQUENCE.  
RX MEDLINE=72062338; PubMed=5126885;  
RA Lote C.J., Weiss J.B.;  
RT "Identification in urine of a low-molecular-weight highly polar  
RT glycopeptide containing cysteinyl-galactose."  
RL Biochem. J. 123:25P-25P(1971).  
CC -1- FUNCTION: The identity of the glycoprotein from which this peptide  
CC is derived is unknown. No physiological function has been  
CC attributed. An erythrocyte membrane glycopeptide having a  
CC similar structure has also been found.  
DR PIR; A03188; XGHUHU.

DR GO; GO:0005576; C:extracellular; NAS.  
KW Glycoprotein.  
FT CARBOHYD 1  
SQ SEQUENCE 8 AA, 855 MW, C2D87AA1F5B1EB1E CRC64;

Query Match 36.0%; Score 9; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 XH 7  
:|  
Db 2 EH 3

## RESULT 9

LCK6\_LEUMA STANDARD; PRT; 8 AA.  
ID LCK6\_LEUMA  
AC P21143;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Leucokinin IV (L-IV).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberridae; Leucophaea.  
NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Head;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Primary structure and synthesis of two additional neuropeptides  
RT from Leucophaea maderae: members of a new family of  
RT cephalomyotropic.";  
RL Comp. Biochem. Physiol. 84C:271-276(1986).  
CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile  
CC activity of cockroach proctodaeum (hindgut).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 8  
SQ SEQUENCE 8 AA, 906 MW, DC635B1B95BDDA CRC64;  
Query Match 36.0%; Score 9; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 XH 7  
:|  
Db 4 FH 5

## RESULT 10

LCK6\_LEUMA STANDARD; PRT; 8 AA.  
ID LCK6\_LEUMA  
AC P19988;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Leucokinin VI (L-VI).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberridae; Leucophaea.  
NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Head;  
RX MEDLINE=87052651; PubMed=2877794;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:  
RT myotonic peptides of Leucophaea maderae.";  
RL Comp. Biochem. Physiol. 88C:27-30(1987).  
CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile

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CC activity of cockroach proctodeum (hindgut).
CC -1- SUBCELLULAR LOCATION: Secreted.
DR PIR; JS0316; JS0316.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 AMIDATION.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 935 MW; 9D635B1E9D5A5A6 CRC64;

Query Match
Best Local Similarity 36.0%; Score 9; DB 1; Length 8;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 XH 7
Db 4 FH 5

RESULT 11
ACT_CARMA STANDARD; PRT; 8 AA.
ID ACT_CARMA
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin (Fragment).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
RA Bachassarian D.;
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
RT Endocrine 5:23-32(1996).
CC -1- FUNCTION: Actins are highly conserved proteins that are involved
CC in various types of cell motility and are ubiquitously expressed
CC in all eukaryotic cells.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS PROTEIN IS:
CC 6.8. ITS MW IS: 46 kDa.
CC -1- SIMILARITY: Belongs to the actin family.
DR InterPro; IPR004001; Actin.
DR PROSITE; PS00406; ACTINS_1; PARTIAL.
DR PROSITE; PS00432; ACTINS_2; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW Structural protein.
FT NON_TER 1 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAB3 CRC64;

Query Match
Best Local Similarity 32.0%; Score 8; DB 1; Length 8;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 OXVX 6
Db 1 KCDVD 5

RESULT 12
AL17_CARMA STANDARD; PRT; 8 AA.
ID AL17_CARMA
AC P81870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas (Common shore crab) (Green crab).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

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OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Jørgensen A.H., Maestro J.-L., Scott A.G., Jaro P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8 8 AMIDATION (POTENTIAL).
SQ SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;

Query Match
Best Local Similarity 32.0%; Score 8; DB 1; Length 8;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XQXX 4
Db 2 GQXS 5

RESULT 13
B44K_PORGI STANDARD; PRT; 8 AA.
ID B44K_PORGI
AC P818E6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 44 kDa immunogenic protein (Fragment).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE.
RC STRAIN=VJB 3492;
RX MEDLINE=20198497; PubMed=10731616;
RA Norris J.W., Love D.N.;
RT "Serum antibody responses of cats to soluble whole cell antigens of
RT feline Porphyromonas gingivalis.";
RL Vet. Microbiol. 73:37-49(2000).
CC -1- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
KW Antigen.
FT NON_TER 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match
Best Local Similarity 32.0%; Score 8; DB 1; Length 8;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XQXX 4
Db 3 YQKR 6

RESULT 14
CLP_THICU STANDARD; PRT; 8 AA.
ID CLP_THICU
AC P80488;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chemolichocroph-specific protein (Fragment).
OS Thiodacillus cuprinus.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Thiomonas.
OX NCBI_TaxID=36860;
RN [1]

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RP SEQUENCE.
RC STRAIN=DSM 5494;
RL MARIN I., Amaro A.M., Jerez C.A., Amile R., Abad J.P.;
RU Submitted (SSP-1995) to Swiss-Pro.
CC -1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
CC CHEMOLITHOTROPHICALLY.
FT NON TER 8
SQ SEQUENCE 8 AA; 785 MW; 91487806DDCD76D CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXX 4
DB 4 ADEG 7

RESULT 15
LCK3 LEUMA
ID LCK3 LEUMA STANDARD; PRT; 8 AA.
AC P2112;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE Leucokinin III (L-III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxId=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of two additional neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotroptins.";
RL Comp. Biochem. Physiol. 84C:271-276(1986).
CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach proctodeum (hindgut).
CC -1- SUBCELLULAR LOCATION: Secreted.
KM Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 910 MW; DC6365B49C866DA CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXX 4
DB 1 DQGF 4

RESULT 16
NPMB BOVIN
ID NPMB BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE Morphine modulating neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX MEDLINE=8067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;

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RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RU Proc. Natl. Acad. Sci. U.S.A. 82:757-776(1985).
CC -1- FUNCTION: Modulates the action of morphine.
CC -1- SUBCELLULAR LOCATION: Secreted.
DR PIR; B24749; B24749.
KM Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXX 4
DB 3 FOPQ 6

RESULT 17
UC26 MAIZE
ID UC26 MAIZE STANDARD; PRT; 8 AA.
AC P80632;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
DE (fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxId=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huot J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 7.0, its MW is: 57.2 kDa.
DR Maize-2DPAGE; P80632; COLEOPTILE.
FT NON TER 1
FT MOD RES 8
SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 32.0%; Score 8; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXX 4
DB 5 DQFK 8

RESULT 18
UF06 MOUSE
ID UF06 MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE Unknown protein from 2D-page of fibroblasts (P50) (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;

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RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RL using preparative two-dimensional gel electrophoresis.";
CC Electrophoresis 15:735-745(1994)
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.2, its MW is: 50 KDa.
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match
Best Local Similarity 32.0%; Score 8; DB 1; Length 8;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 H 7
DB 1 H 1

RESULT 19
UH09 RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot p9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Miscar; TISSUE=Heart;
RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RL Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 8.9, its MW is: 42 KDa.
FT NON TER 8
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

Query Match
Best Local Similarity 32.0%; Score 8; DB 1; Length 8;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXX 4
DB 4 ROSP 7

RESULT 20
AKHG GRVBI STANDARD; PRT; 8 AA.
ID AKHG GRVBI
AC P14066;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_Taxid=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G. bimaculatus; TISSUE=Corpora cardiaca;
RA MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
RT of a peptide with adipokinetic activity from the corpora cardiaca of
RT the cricket Gryllus bimaculatus.";
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RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R. microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -1- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC PIR, A28004; A28004.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match
Best Local Similarity 28.0%; Score 7; DB 1; Length 8;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4
DB 1 QVN 3

RESULT 21
AKH LIBAU STANDARD; PRT; 8 AA.
ID AKH LIBAU
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_Taxid=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -1- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC PIR, S10596; S10596.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match
Best Local Similarity 28.0%; Score 7; DB 1; Length 8;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4
DB 1 QVN 3
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Db 1 QVN 3

RESULT 22

AKH\_MELML STANDARD; PRT; 8 AA.

AC P25423;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Adipokinetic hormone (AKH).

OS Melolontha melolontha (Cockchafer), and

OS Geotrupes stercorarius (Dor beetle), and

OS Pachnoda marginata (Flower beetle).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;

OC Scarabaeidae; Melolonthinae; Melolontha.

OX NCBI\_TaxID=7061, 7087, 7058;

RN [1]

RP SEQUENCE.

RC SPECIES=M. melolontha, and G. stercorarius; TISSUE=Corpora cardiaca;

RX MEDLINE=91248100; Pubmed=2039445;

RA Gaede G.;

RT "A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and sequenced from two beetle species."

RT Biochem. J. 275:671-677 (1991).

RL [2]

RN SEQUENCE.

RP SPECIES=P. marginata; TISSUE=Corpora cardiaca;

RX MEDLINE=92265187; Pubmed=1586453;

RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;

RT "Primary structures of neuropeptides isolated from the corpora cardiaca of various cetonid beetle species determined by pulsed-liquid phase sequencing and tandem fast atom bombardment mass spectrometry."

RT Biol. Chem. Hoppe-Seyler 373:133-142 (1992).

RL -1- FUNCTION: This hormone, released from cells in the corpora cardiaca after the beginning of flight, causes release of diglycerides from the fat body and then stimulates the flight muscles to use these diglycerides as an energy source.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.

DR PIR: A58641; A58641.

DR PIR: S15422; S15422.

DR PIR: S21663; S21663.

DR InterPro: IPR002047; AKH.

DR PROSITE: PS00256; AKH, 1.

KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 8 PYRROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 8 8 AMIDATION.

FT SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;

QY 2 QXX 4

Db 1 QLN 3

Query Match 28.0%; Score 7; DB 1; Length 8;

Best Local Similarity 33.3%; Pred. No. 1.4e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 23

AKH\_TABAT STANDARD; PRT; 8 AA.

AC P14595;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I) (DCC I).

OS Tabanus atratus (Horse fly).

OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;

OC Tabanus.

OX NCBI\_TaxID=7207;

RN [1]

RP SEQUENCE.

RC TISSUE=Corpora cardiaca;

RX MEDLINE=90046758; Pubmed=2813385;

RA Jaffe H., Raina A.K., Riley C.T., Frazer B.A., Nachman R.J., Vogel V.W., Zhang Y.-S., Hayes D.K.;

RT "Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activity isolated from the corpora cardiaca of horse flies (Diptera)."

RT Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).

RL -1- FUNCTION: This hormone, released from cells in the corpora cardiaca after the beginning of flight, causes release of diglycerides from the fat body and then stimulates the flight muscles to use these diglycerides as an energy source.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.

DR PIR: A33995; A33995.

DR InterPro: IPR002047; AKH.

DR PROSITE: PS00256; AKH, 1.

KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 8 PYRROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 8 8 AMIDATION.

FT SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

QY 2 QXX 4

Db 1 QLT 3

Query Match 28.0%; Score 7; DB 1; Length 8;

Best Local Similarity 33.3%; Pred. No. 1.4e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 24

CAD1\_ENTFA STANDARD; PRT; 8 AA.

AC P13268;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1991 (Rel. 17, Last annotation update)

DE Sex pheromone CAD1.

OS Enterococcus faecalis (Streptococcus faecalis).

OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OX NCBI\_TaxID=1351;

RN [1]

RP SEQUENCE.

RX MEDLINE=85051889; Pubmed=6437873;

RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C., Craig R.A., Clewell D.B., Suzuki A.;

RT "Isolation and structure of the bacterial sex pheromone, CAD1, that induces plasmid transfer in Streptococcus faecalis."

RL FBS Lett. 178:97-100 (1984).

CC -1- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMOLYSIN PLASMID PAD1.

KW Pheromone.

FT SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

QY 3 XXVX 6

Db 3 SLVL 6

Query Match 28.0%; Score 7; DB 1; Length 8;

Best Local Similarity 25.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 25

COM2\_CONFU STANDARD; PRT; 8 AA.

AC P58785;

DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leu-contryphan-P.  
 OS Conus purpurascens (Purple cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 NCBI\_TaxId=41690;  
 (1)  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC STRAIN-Clipperton Island; TISSUE=Venom;  
 RX MEDLINE=99388839; PubMed=10461743;  
 RA Jacobsen R.B.; Jimenez E.C.; De la Cruz R.G.C.; Gray W.R.; Cruz L.J.;  
 RA Olivera B.M.;  
 RT "A novel D-leucine-containing Conus peptide: diverse conformational  
 RT dynamics in the contryphan family."  
 RL J. Pept. Res. 54:93-99(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.  
 CC -1- SIMILARITY: Belongs to the contryphan family.  
 KW Toxin; Hydroxylation; D-amino acid.  
 FT DISUFID 2 8  
 FT MOD RES 4 4  
 FT SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVX 6  
 : : :  
 DB 1 GCVL 4

RESULT 26  
 ID FARA4 MACRS STANDARD; PRT; 8 AA.  
 AC P83277;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRamide-like neuropeptide FLp4 (APALRLP-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 NCBI\_TaxId=79674;  
 (1)  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sithigorngul P.; Sarathongkum W.; Jaidechoy S.; Longyant S.;  
 RA Sithigorngul W.;  
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii.";  
 RL Comp. Biochem. Physiol. 120B:587-595(1998).  
 CC -1- MASS SPECTROMETRY: MW=943; METHOD=WALDI.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.  
 GO: GO:0007218; P:neuropeptide signaling pathway; TAS.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8 8  
 FT SEQUENCE 8 AA; 943 MW; 9CD40734072DC76D CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 XXVXHL 8  
 : : :  
 DB 1 APALRL 6

RESULT 27  
 ID HTFL PERAM STANDARD; PRT; 8 AA.  
 AC P04548;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplanetin CC-1)  
 DE (Pea-CAH-1) (Led-CC-1) (Hypertrehalosaemic neuropeptide I).  
 OS Periplaneta americana (American cockroach).  
 OS Leptinocara decemlineata (Colorado potato beetle), and  
 OS Blatta orientalis (Oriental cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 NCBI\_TaxId=6978, 7539, 6976;  
 (1)  
 RP SEQUENCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=85046530; PubMed=6548628;  
 RA Wilten J.L.; Schaffer M.H.; O'Shea M.; Cook J.C.; Hemling M.E.;  
 RA Rinehart K.L., Jr.;  
 RT "Structures of two cockroach neuropeptides assigned by fast atom  
 RT bombardment mass spectrometry."  
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=84298179; PubMed=6591205;  
 RA Scarborough R.M.; Jamieson G.C.; Kallish F.; Kramer S.J.; McEnroe G.A.;  
 RA Miller C.A.; Schooley D.A.;  
 RT "Isolation and primary structure of two peptides with  
 RT cardioacceleratory and hyperglycemic activity from the corpora  
 RT cardiaca of Periplaneta americana."  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;  
 RX MEDLINE=90160053; PubMed=2576128;  
 RA Gaede G.; Kellner R.;  
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato  
 RT beetle and the American cockroach are identical."  
 RL Peptides 10:1287-1289(1989).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;  
 RX MEDLINE=90253659; PubMed=2340112;  
 RA Gaede G.; Rinehart K.L., Jr.;  
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from  
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,  
 RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis  
 RT and of the stick insect Exaltosoma tilatuma assigned by tandem fast  
 RT atom bombardment mass spectrometry."  
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
 CC -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that  
 CC elevate the level of trehalose in the hemolymph (trehalose is  
 CC the major carbohydrate in the hemolymph of insects).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
 CC PIR; A05169; A05169.  
 DR PIR; A44960; A44960.  
 DR PIR; A49823; A49823.  
 DR PIR; S08995; S08995.  
 DR InterPro: IPR002047; AKH.  
 DR PROSITE: PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1  
 FT MOD RES 8 8  
 FT SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;

Qy	Matches	1: Conservative	2: Mismatches	0: Indels	0: Gaps
Qy	2 QXX 4				
Db	1 QVN 3				
RESULT: 28					
ID	HTF2_PERAM	STANDARD:	PRT:	8 AA.	
AC	P04549;				
DT	13-AUG-1987 (Rel. 05, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Hypertrihaloaemic factor II (Neuropeptide M-II) (Periplanetin CC-2)				
DE	(PeA-CAH-II) (Leb-CC-II) (Hypertrihaloaemic neuropeptide II).				
OS	Periplaneta americana (American cockroach),				
OS	Leptinotarsa decemlineata (Colorado potato beetle), and				
OS	Blattella orientalis (Oriental cockroach).				
OC	Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,				
OC	Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;				
OC	Blattidae; Periplaneta.				
OX	NCBI_TaxID=6978, 7539, 6976;				
RP	SEQUENCE.				
RC	SPECIES=P.americana;				
RC	MEDLINE=55046530; PubMed=6548628;				
RA	Walten J.L., Schaffner M.H., O'Shea M., Cook J.C., Hemling M.E.,				
RA	Rinehart K.L. Jr.;				
RT	"Structures of two cockroach neuropeptides assigned by fast atom				
RT	bombardment mass spectrometry.";				
RL	Biochem. Biophys. Res. Commun. 124:350-358(1984).				
RN	[2]				
RP	SEQUENCE.				
RC	SPECIES=P.americana;				
RC	MEDLINE=84298179; PubMed=6591205;				
RX	Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McIntire G.A.,				
RA	Miller C.A., Schooley D.A.;				
RT	"Isolation and primary structure of two peptides with				
RT	cardioacceleratory and hyperglycemic activity from the corpora				
RT	cardica of Periplaneta americana.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).				
RN	[3]				
RP	SEQUENCE.				
RC	SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;				
RC	MEDLINE=90160053; PubMed=2576128;				
RX	Gaede G., Rinehart R.;				
RA	"The metabolic neuropeptides of the corpus cardiacum from the potato				
RT	beetle and the American cockroach are identical.";				
RL	Peptides 10:1287-1289(1989).				
RN	[4]				
RP	SEQUENCE.				
RC	SPECIES=B.orientalis; TISSUE=Corpora cardiaca;				
RC	MEDLINE=90253659; PubMed=2340112;				
RX	Gaede G., Rinehart K.L. Jr.;				
RA	"Primary structures of hypertrihaloaemic neuropeptides isolated from				
RT	the corpora cardiaca of the cockroaches Leucophaea maderae,				
RT	Gromphodroma portoricensis, Blattella germanica and Blattella orientalis				
RT	and of the stick insect Extradosoma tatarum assigned by tandem fast				
RT	atom bombardment mass spectrometry.";				
RL	Biol. Chem. Hoppe-Seyler 371:345-354(1990).				
CC	-1- FUNCTION: Hypertrihaloaemic factors are neuropeptides that				
CC	elevate the level of trehalose in the hemolymph of insects.				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- SIMILARITY: Belongs to the AKH / HRTA / RPCH family.				
DR	PIR; B44960; B44960.				
DR	PIR; B49823; B49823.				
DR	PIR; S08996; S08996.				
DR	InterPro; IPR002047; AKH.				
DR	PROSITE; PS00256; AKH; 1.				
KM	Neuropeptide; Amidation; Pyrrolidone carboxylic acid.				
RT	MOD_RSS 1 1 PYRROLIDONE CARBOXYLIC ACID.				

[illegible]

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RC TISSUE=Corpora cardiaca;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin II, an
RT additional neuropeptide of Locusta migratoria. Member of the
RT cephalomyotropic peptide family.";
RL Insect Biochem. 20:479-484(1990).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotrophic
CC activity).
CC -1- SIMILARITY: Belongs to the pyrokinin family.
CC Interpro: IPR001484; PYROKININ.
DR PROSITE: PS00539; PYROKININ; 1.
KM Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 8 AA; 934 MW; 26341771A9CA87B CRC64;
SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 16.7%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 XXVXHL 8
DB 3 DTPRL 8

RESULT 31
LPK_LEUMA STANDARD; PRT; 8 AA.
ID LPK_LEUMA
AC P13049;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leukopyrokinin (LPK) (LEW-PK).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Leucophaea.
OC NCBI_Taxid=6988;
OX (1)
RN
RP SEQUENCE.
RX MEDLINE=86269041; PubMed=3015140;
RA Nachman R.J., Holman G.M., Cook B.J.;
RT "Active fragments and analogs of the insect neuropeptide
RT leucopyrokinin: structure-function studies.";
RL Biochem. Biophys. Res. Commun. 137:936-942(1986).
RN (2)
RN SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Primary structure and synthesis of a blocked myotropic
RT neuropeptide isolated from the cockroach, Leucophaea maderae.";
RL Comp. Biochem. Physiol. 85C:219-224(1986).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotrophic
CC activity).
CC -1- MISCELLANEOUS: An analog without the N-terminal PCA residue was
CC synthesized and found to exhibit greater activity (144%) than the
CC parent neuropeptide. The portion of the sequence of LPK most
CC critical for the myotropic properties is limited to the
CC pentapeptide fragment FTRPL.
CC -1- SIMILARITY: Belongs to the pyrokinin family.
DR PIR: A23967; A23967.
DR Interpro: IPR001484; PYROKININ.
DR PROSITE: PS00539; PYROKININ; 1.
KM Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXX 4

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DB 1 QTS 3

RESULT 32
PLP_BRANA STANDARD; PRT; 8 AA.
ID PLP_BRANA
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Placental lipid-associated protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Brassica.
OX NCBI_Taxid=3708;
RN (1)
RN
RP SEQUENCE.
RC STRAIN=CV. TOPAZ; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;
RA Hernandez-Pinzon I., Rose J.H.E., Barnes K.A., Damant A.P.,
RA Murphy D.J.;
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RT pollen coat of Brassica napus.";
RL Planta 208:588-598(1999).
CC -1- FUNCTION: May play a structural role in the elaioplast, a tapetum-
CC specific plastidial lipid organelle.
CC -1- TISSUE SPECIFICITY: Tapetum of anthers.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CA042 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVX 6
DB 2 IDVN 5

RESULT 33
PPK2_PBRAM STANDARD; PRT; 8 AA.
ID PPK2_PBRAM
AC P82632;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattaria; Periplaneta.
OX NCBI_Taxid=6978;
RN (1)
RN
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN (2)
RN TISSUE SPECIFICITY.
RP MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotrophic
CC activity).
CC -1- TISSUE SPECIFICITY: Corpora cardiaca.
CC -1- MASS SPECTROMETRY: MW=883; METHOD=MALDI.

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CC -1- SIMILARITY: Belongs to the pyrokinin family.  
 DR InterPro: IPR001484; Pyrokinin.  
 DR ProSITE: PS00539; PYROKININ; FALSE\_NEG.  
 KM Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 8  
 SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 XXVXHL 8  
 Db 3 PFAPRL 8

RESULT 34  
 RPCH\_PANBO STANDARD; PRT; 8 AA.  
 AC P08939;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Red pigment concentrating hormone (RPCH).  
 OS Pandanus borealis (Northern red shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidae;  
 OC Pandalidae; Pandalus.  
 OX NCBI\_TaxID=6703;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75054965; PubMed=4433569;  
 RA Fernlund P.;  
 RT "Structure of the red-pigment-concentrating hormone of the shrimp,  
 Pandanus borealis.";  
 RL Biochim. Biophys. Acta 371:304-311(1974).  
 CC -1- FUNCTION: This hormone adapts the animal to light backgrounds by  
 stimulating concentration of the pigment of its red body-  
 chromophores.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
 DR InterPro: IPR002047; AKH.  
 DR ProSITE: PS00256; AKH; 1.  
 KM Pigment; Hormone; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1  
 FT MOD\_RES 8  
 FT MOD\_RES 1  
 SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QXX 4  
 Db 1 QLN 3

RESULT 35  
 VGLG\_HSV2B STANDARD; PRT; 8 AA.  
 AC P81809;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Glycoprotein G (Fragment).  
 OS Herpes simplex virus (type 2 / strain B4327UR).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=103921;  
 RN [1]  
 RP SEQUENCE.  
 RA Liljegvist J.-A., Svennerholm B., Bergstrom T.;

RL Submitted (APR-1999) to Swiss-Prot.  
 CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND  
 CC 2: GH, GB, GC, GD, GI, AND GE.  
 CC -1- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN  
 CC HSV-1.  
 KM Glycoprotein.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 683 MW; 7B47686772C865B8 CRC64;

Query Match 28.0%; Score 7; DB 1; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVX 6  
 Db 2 SGVP 5

RESULT 36  
 AL12\_CARMA STANDARD; PRT; 8 AA.  
 AC P81815;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinus maenas 12.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.  
 CC -1- SIMILARITY: Belongs to the allostatin family.  
 KM Neuropeptide; Multigene family.  
 SQ SEQUENCE 8 AA; 913 MW; 672879CDBC569AB7 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 12.5%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 XQXXVXHL 8  
 Db 1 PDWYAFGL 8

RESULT 37  
 ALL7\_CARMA STANDARD; PRT; 8 AA.  
 ID ALL7\_CARMA  
 AC P81809; P81804; P81810;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Carcinus maenas 7 [Contains: Carcinustatin 6; Carcinustatin 1].  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;

```

RT "Isolation and identification of multiple neuropeptides of the
RL allatostatin superfamily in the shore crab Carcinus maenas.";
RC Bur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation; Multigene family.
FT PEPTIDE 1 8 CARCINOSTATIN 7.
FT PEPTIDE 2 8 CARCINOSTATIN 6.
FT PEPTIDE 4 8 CARCINOSTATIN 1.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 825 MW; 922879CDCB4775BD CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
Best Local Similarity 12.5%; Pred. No. 1.4e+05;
Matches 1; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 XQXXVXL 8
DB 1 ASPYAFGL 8

RESULT 38
FAR1_PENMO STANDARD; PRT; 8 AA.
AC P83316;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLPI (GDRNFLRF-amide).
OS Pennaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Pennaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; Pubmed=11959015;
RA Sithigornngul P., Pupuem J., Krungkassam C., Longyant S.,
RA Chaiyavithangskura P., Sithigornngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Pennaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO:0007218; P-neuropeptide signaling pathway; TMS.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540A8 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
Best Local Similarity 0.0%; Pred. No. 1.4e+05;
Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
DB 2 DRRFLR 7

RESULT 39
FAR2_MACRS STANDARD; PRT; 8 AA.
AC P83275;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLPI2 (ADKXFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.

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OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigornngul P., Sarathongkum W., Jaidechoey S., Longyant S.,
RA Sithigornngul W.;
RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -1- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO:0007218; P-neuropeptide signaling pathway; TMS.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
Best Local Similarity 0.0%; Pred. No. 1.4e+05;
Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
DB 2 DRRFLR 7

RESULT 40
FAR3_HOMAM STANDARD; PRT; 8 AA.
AC P41486;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide 3 (FLI 3) (F2).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=88116164; Pubmed=3429714;
RA Trimmer B.A., Koblitzki L.A., Kravitz E.A.;
RT "Purification and characterization of FMRamide-like immunoreactive
RT substances from the lobster nervous system: isolation and sequence
RT analysis of two closely related peptides.";
RL J. Comp. Neurol. 266:16-26(1987).
CC -1- MISCELLANEOUS: Pericardial organs release this peptide with 100 nm
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;
Best Local Similarity 0.0%; Pred. No. 1.4e+05;
Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
DB 2 DRRFLR 7

RESULT 41
FAR4_HOMAM STANDARD; PRT; 8 AA.
AC P41487;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide 4 (FLI 4) (F1).

```

OS Homarus americanus (American lobster).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Nephropidae; Nephropidae; Homarus.  
 RX NCBI\_TaxID=6706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=88116164; PubMed=3429714;  
 RA Trimmer B.A., Kobler E.A., Kravitz E.A.;  
 RT "Purification and characterization of FMRFamide-like immunoreactive  
 substances from the lobster nervous system: isolation and sequence  
 analysis of two closely related peptides.";  
 RL J. Comp. Neurol. 266:16-26(1987).  
 CC -1- FUNCTION: Can act as a modulator of exoskeletal and cardiac  
 neuromuscular junctions.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 family.  
 CC Neuropeptide; Amidation.  
 KM MOD RES 8  
 FT SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;  
 SQ  
 Query Match 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXX 6  
 DB 2 NRNFRL 7

RESULT 42  
 FARP7\_ASCSU STANDARD; PRT; 8 AA.  
 ID FARP7\_ASCSU  
 AC P43171;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE FMRFamide-like neuropeptide AF7.  
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;  
 OC Ascarididae; Ascaris.  
 RX NCBI\_TaxID=6253;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95380362; PubMed=7651904;  
 RA Cowden C., Stretton A.O.W.;  
 RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode  
 Ascaris suum.";  
 RL Peptides 16:491-500(1995).  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 family.  
 CC Neuropeptide; Amidation.  
 KM MOD RES 8  
 FT SEQUENCE 8 AA; 963 MW; 9CD40059D41687D CRC64;  
 SQ  
 Query Match 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXXX 6  
 DB 4 RFR 7

RESULT 43  
 NS3\_MYCTU STANDARD; PRT; 8 AA.  
 ID NS3\_MYCTU  
 AC P81152;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 30 kDa non-secretory protein 3 (Fragment).

OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacteriineae; Mycobacteriaceae; Mycobacterium.  
 RX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=H37Rv;  
 RA Prasad H.K., Annapurna P.S.;  
 RL Submitted (DEC-1997) to Swiss-Prot.  
 CC -1- CAUTION: We are unable to find this protein in the translation of  
 the genome of strain H37Rv.  
 CC NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 919 MW; 8D3DC40B19CDC2D2 CRC64;  
 Query Match 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VXX 6  
 DB 1 VVA 3

RESULT 44  
 PPK3\_PERAM STANDARD; PRT; 8 AA.  
 ID PPK3\_PERAM  
 AC P82618;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-3 (Pea-PK-3) (PYPRL-amide).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattellidae;  
 OC Blattidae; Periplaneta.  
 RX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Retrocerebral complex;  
 RX MEDLINE=99212469; PubMed=10196736;  
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
 RT "Differential distribution of pyrokinin-isoforms in cerebral and  
 abdominal neurohemal organs of the American cockroach.";  
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).  
 RN [2]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "A gamma-specific distribution of PXPRLamides in the nervous system of  
 the American cockroach.";  
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
 activity).  
 CC -1- TISSUE SPECIFICITY: Corpora cardiaca.  
 CC -1- MASS SPECTROMETRY: MW=996.5; METHOD=MLDI.  
 CC -1- SIMILARITY: Belongs to the pyrokinin family.  
 CC Neuropeptide; Amidation; Pyrokinin.  
 KM MOD RES 8  
 FT SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;  
 SQ  
 Query Match 24.0%; Score 6; DB 1; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VXX 6  
 DB 1 LVP 3

RESULT 45  
 RT34\_BOVIN STANDARD; PRT; 8 AA.  
 ID RT34\_BOVIN

AC P82929;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).  
 GN MRP834.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxId=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=21276436; PubMed=11279123;  
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremull L.L.;  
 RT "The small subunit of the mammalian mitochondrial ribosome:  
 RT identification of the full complement of ribosomal proteins present.";  
 RL J. Biol. Chem. 276:19363-19374(2001).  
 CC -1- SUBUNIT: Component of the mitochondrial ribosome small subunit  
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 KW Ribosomal protein; Mitochondrion.  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 24.0%; Score 6; DB 1; Length 8;

Best Local Similarity 0.0%; Pred. No. 1.4e+05; Mismatches 0; Indels 0; Gaps 0;

OY 3 XXVX 6  
 : : :  
 DB 2 WGIL 5

Search completed: August 19, 2004, 15:51:48  
 Job time : 8 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 19, 2004, 15:47:57 ; Search time 31 Seconds  
(without alignments)  
81.424 Million cell updates/sec

Title: VARIANT1

Perfect score: 25

Sequence: 1 XQXXVH 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues 414

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL.25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	15	60.0	8	Q7Z6G0	Q7Z6G0 homo sapien
2	14	56.0	8	Q91098	Q91098 manorina me
3	14	56.0	8	Q90498	Q90498 erythrura g
4	13	52.0	8	P72279	P72279 rhodococcus
5	13	52.0	8	Q9UMC7	Q9UMC7 homo sapien
6	13	52.0	8	Q9XSY1	Q9XSY1 canis famil
7	13	52.0	8	Q8WGC9	Q8WGC9 upogebia af
8	12	48.0	8	Q9ZEZ9	Q9ZEZ9 buchiera ap
9	12	48.0	8	O56246	O56246 thermophili
10	12	48.0	8	Q8G940	Q8G940 borrelia bu
11	12	48.0	8	P83152	P83152 anabena sp
12	12	48.0	8	Q9TWH6	Q9TWH6 perineleis
13	12	48.0	8	Q34909	Q34909 locusta mig
14	12	48.0	8	Q37854	Q37854 bacterioph
15	12	48.0	8	P87488	P87488 oncorhynch
16	12	48.0	8	P82082	P82082 limodynast

17	11	44.0	8	Q15894	Q15894 homo sapien
18	11	44.0	8	Q9UDZ4	Q9UDZ4 homo sapien
19	11	44.0	8	Q9UMH9	Q9UMH9 homo sapien
20	11	44.0	8	O15899	O15899 babesia ovi
21	11	44.0	8	P79940	P79940 xenopus lae
22	11	44.0	8	P82083	P82083 limodynast
23	10	40.0	8	Q45615	Q45615 bacillus eu
24	10	40.0	8	P77556	P77556 escherichia
25	10	40.0	8	Q93SP2	Q93SP2 pseudomonas
26	10	40.0	8	O8G121	O8G121 borrelia bu
27	10	40.0	8	O13591	O13591 saccharomyc
28	10	40.0	8	Q9BRT5	Q9BRT5 homo sapien
29	10	40.0	8	Q15893	Q15893 homo sapien
30	10	40.0	8	O8IUB8	O8IUB8 homo sapien
31	10	40.0	8	O8MUN6	O8MUN6 heliconius
32	10	40.0	8	O02032	O02032 lytechinus
33	10	40.0	8	O8EBS9	O8EBS9 strongyloc
34	10	40.0	8	Q9T778	Q9T778 canis famil
35	10	40.0	8	Q9BFR2	Q9BFR2 ursus arcto
36	10	40.0	8	Q9BFC2	Q9BFC2 macropus eu
37	10	40.0	8	Q9BFR9	Q9BFR9 tragalaphus
38	10	40.0	8	Q9BFR1	Q9BFR1 echinops te
39	10	40.0	8	Q9BFR1	Q9BFR1 atelax fusc
40	10	40.0	8	Q9BFR7	Q9BFR7 capitis ind
41	10	40.0	8	Q9BFR9	Q9BFR9 euphractus
42	10	40.0	8	Q9BFR8	Q9BFR8 chaetophrac
43	10	40.0	8	Q9BFR0	Q9BFR0 macaca mula
44	10	40.0	8	Q9BFR8	Q9BFR8 loxodonta a
45	10	40.0	8	Q9BFR9	Q9BFR9 procavia ca

#### ALIGNMENTS

RESULT 1	Q7Z6G0	PRELIMINARY;	PRT;	8 AA.
ID	Q7Z6G0			
AC	Q7Z6G0;			
DT	01-OCT-2003 (TREMBLrel. 25, Created)			
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Fumarate hydratase (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Wei M.-H., Nickerson M.L., Toro J.R.;			
RT	"dinucleotide repeat polymorphisms in the fumarate hydratase gene of			
RT	human chromosome 1q42.3."			
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY29638; AAF57532.1; -			
FT	NON TER			
FT	NON TER			
SQ	SEQUENCE 8 AA; 881 MW; 40CSBIE732C44330 CRC64;			
Query Match	Best Local Similarity	60.0%;	Score 15;	DB 4; Length 8;
Matches	2; Conservative	40.0%;	Pred. No. 1e+06;	
		3; Mismatches	0; Indels	0; Gaps 0;
QY	3 XQXXH 7			
Db	2 KNYLH 6			
RESULT 2	Q91098	PRELIMINARY;	PRT;	8 AA.
ID	Q91098			
AC	Q91098;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)			

DE Myoglobin (Fragment).  
 OS Manorina melanoccephala (Noisy miner).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Meliphagidae; Manorina.  
 NCBI\_TaxID=44314;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=D02;  
 RX MEDLINE=98208049; PubMed=9548272;  
 RA Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;  
 RT "Myoglobin intron variation in the Gouldian Finch *Erythrura gouldiae*  
 assessed by temperature gradient gel electrophoresis.";  
 RL Electrophoresis 19:142-151(1998).  
 DR EMBL; U40497; AAC60364.1; -.  
 FT NON\_TER 1 8  
 SQ SEQUENCE 8 AA; 890 MW; C6C1F2C865B046DE CRC64;

Query Match 56.0%; Score 14; DB 13; Length 8;  
 Best Local Similarity 28.6%; Pred. No. 1e+06;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XXXXXVH 7  
 :|:::|  
 DB 1 CQISGVH 7

RESULT 3  
 ID 090498 PRELIMINARY; PRT; 8 AA.  
 AC 090498;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
 DE Myoglobin (Fragment).  
 OS Erythrura gouldiae (Gouldian finch).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidae; Passeridae;  
 OC Erythrura.  
 NCBI\_TaxID=44316;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EGG1;  
 RX MEDLINE=98208049; PubMed=9548272;  
 RA Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;  
 RT "Myoglobin intron variation in the Gouldian Finch *Erythrura gouldiae*  
 assessed by temperature gradient gel electrophoresis.";  
 RL Electrophoresis 19:142-151(1998).  
 DR EMBL; U40496; AAC60363.1; -.  
 FT NON\_TER 1 8  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 890 MW; C6C1F2C865B046DE CRC64;

Query Match 56.0%; Score 14; DB 13; Length 8;  
 Best Local Similarity 28.6%; Pred. No. 1e+06;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XXXXXVH 7  
 :|:::|  
 DB 1 CQISGVH 7

RESULT 4  
 ID P72279 PRELIMINARY; PRT; 8 AA.  
 AC P72279;  
 DT 01-FEB-1997 (TReMBLrel. 02, Created)  
 DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Biphenyl dioxygenase (Fragment).  
 BPHB.  
 GN Rhodococcus globerulus.  
 OS Rhodococcus globerulus.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Nocardiaceae; Rhodococcus.  
 NCBI\_TaxID=33008;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95255652; PubMed=7737502;  
 RA Asturias J.A., Diaz E., Timmis K.N.;  
 RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-  
 positive bacterium *Rhodococcus globerulus* p6 to multicomponent  
 dioxygenases of gram-negative bacteria.";  
 RL Gene 156:11-18(1995).  
 DR EMBL; X80041; CAA56350.1; -.  
 DR GO; GO:0016702; Peroxidoreductase activity, acting on single d. .; IEA.  
 KW Dioxygenase.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;

Query Match 52.0%; Score 13; DB 2; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1e+06;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXVX 6  
 :|:::|  
 DB 3 LODEVY 8

RESULT 5  
 ID 09UMC7 PRELIMINARY; PRT; 8 AA.  
 AC 09UMC7;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
 DE SHMT protein (Fragment).  
 GN SHMT.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Chave K.J., Snell K., Sanders P.G.;  
 RT "Isolation and characterisation of human genomic sequences encoding  
 cytosolic serine hydroxymethyltransferase.";  
 RL Biochem. Soc. Trans. 25:53-53(1997).  
 DR EMBL; Y14492; CAB54844.1; -.  
 FT NON\_TER 1 8  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 868 MW; 7C205721B44AB5B8 CRC64;

Query Match 52.0%; Score 13; DB 4; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHL 8  
 :|||  
 DB 4 NHL 6

RESULT 6  
 ID 09XSY1 PRELIMINARY; PRT; 8 AA.  
 AC 09XSY1;  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)  
 DE Retinoblastoma protein (Fragment).  
 RB1.  
 GN Canis familiaris (Dog).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 NCBI\_TaxID=9615;  
 RN (1)  
 RP SEQUENCE FROM N.A.

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RX MEDLINE=97049323; PubMed=8894053;
RA Venter P.J., Brocchieri J.A., Yuzbasiyan-Gurkan V., Brewer G.J.;
RT "Gene-specific universal mammalian sequence-tagged sites: application
to the canine genome.";
RL Biochem. Genet. 34:321-341(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Venter P.J., Cao Y., Alexander L., Yuzbasiyan-Gurkan V.;
RT "Dinucleotide repeat polymorphism in the canine retinoblastoma (Rb1)
gene.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF155737; AAD38807.1; -.
FT NON TER 1 1
SQ SEQUENCE 8 AA; 895 MW; 1425B818676721E3 CRC64;

Query Match 52.0%; Score 13; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHL 8
DB 1 KHL 3

RESULT 7
O8WGC9 PRELIMINARY; PRT; 8 AA.
ID O8WGC9
AC O8WGC9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
OS Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Thalassinidea;
OC Callinassoidae; Upogebiidae; Upogebia.
OC NCBI_TaxID=177247;
RN [1]
RP SEQUENCE FROM N.A.
RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
RA Cunningham C.W.;
RT "Mitochondrial gene rearrangements support a hypothesis of parallel
evolution to the crab-like form.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF436047; AA131621.1; -.
DR GO; GO:0005739; Mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 978 MW; FE20573B5452C056 CRC64;

Query Match 52.0%; Score 13; DB 8; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
DB 1 MIVNYL 6

RESULT 8
O9ZEZ9 PRELIMINARY; PRT; 8 AA.
ID O9ZEZ9
AC O9ZEZ9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).
OS LeuA.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

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OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99028904; PubMed=9812361;
RA Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
RT "Structure and evolution of the leucine plasmids carried by the
RT endosymbiont (Buchnera aphidicola) from aphids of the family
RT Aphididae.";
RL FEMS Microbiol. Lett. 168:43-49(1998).
DR EMBL; AJ006874; CA07290.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0003852; F:2-isopropylmalate synthase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase; Plasmid.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 917 MW; FE205042D6C5B446 CRC64;

Query Match 48.0%; Score 12; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 1e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
DB 3 SQVITL 8

RESULT 9
O56246 PRELIMINARY; PRT; 8 AA.
ID O56246
AC O56246; Q52410;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 05, Last sequence update)
DT 01-JAN-1998 (TREMBlrel. 08, Last annotation update)
DE Thermophilic proton ATPase epsilon subunit amino terminal (Fragment).
OS Thermophilic bacterium P53.
OC Bacteria; Firmicutes; Bacillales.
OC NCBI_TaxID=2334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PS3;
RX MEDLINE=87137359; PubMed=2880841;
RA Kagawa Y., Ishizuka M., Saitoh T., Nakao S.;
RT "Stable structure of thermophilic proton ATPase beta subunit.";
RL J. Biochem. 100:923-934(1986).
DR EMBL; D00113; BAA0067.1; -.
DR EMBL; X04609; CAA28278.1; -.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 914 MW; EBD5A2C1B041A336 CRC64;

Query Match 48.0%; Score 12; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 1e+06;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXHL 8
DB 1 MKTIV 6

RESULT 10
O8G940 PRELIMINARY; PRT; 8 AA.
ID O8G940
AC O8G940;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OS Bacteria; Spirochaetes; Spirochaetiales; Spirochaetaceae; Borrelia.
OC Bacteria; Spirochaetes; Spirochaetiales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=DN127c19-2, and Sh-2-82;
RC PLASMID=group cp32-9, and group cp32-12;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT phages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142104; AN17853.1; -.
DR EMBL; AY142097; AN17907.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 8 AA; 1042 MW; 1437244330504373 CRC64;

Query Match 48.0%; Score 12; DB 2; Length 8;
Best Local Similarity 14.3%; Pred. No. 1e+06;
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXHL 8
DB 1 KWIIXNL 7

RESULT 11
ID P83152 PRELIMINARY; PRT; 8 AA.
AC P83152;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Allophycocyanin beta chain (Fragment).
OS Anabaena sp. (Strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxId=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to Swiss-Prot.
CC -1- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
CC FROM THE PHYCOBILIPROTEIN COMPLEX. ALLOPHYCOCYANIN HAS A MAXIMUM
CC ABSORPTION AT APPROXIMATELY 650 TO 653 NANOMETERS.
CC -1- SUBUNIT. HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE.
CC -1- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030089; C:phycobillosome; IEA.
DR GO; GO:0009579; C:thylakoid; IEA.
DR GO; GO:0006119; P:electron transport; IEA.
DR GO; GO:0015979; P:photosynthesis; IEA.
KW Phycobillosome; Electron transport; Photosynthesis; Bile pigment;
KW Thylakoid; Membrane.
FT NON_TER
SQ SEQUENCE 8 AA; 788 MW; 87CDClA05DDAB6DD CRC64;

Query Match 48.0%; Score 12; DB 2; Length 8;
Best Local Similarity 16.7%; Pred. No. 1e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 6
DB 1 AODAIT 6

RESULT 12
ID Q9TWH6 PRELIMINARY; PRT; 8 AA.
AC Q9TWH6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE BIOACTIVE peptide P4=PUTATIVE ESOPHAGEAL NEUROREGULATOR.
OS Perinereis vancaurica.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;
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OC Phylloccida; Nereididae; Perinereis.
OX NCBI_TaxId=6355;
RN [1]
RP SEQUENCE.
RX MEDLINE=95233338; PubMed=7599979;
RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.,
RA Fujita T., Minakata H., Nomoto K.;
RT "Isolation and characterization of four novel bioactive peptides from
RT a polychaete annelid, Perinereis vancaurica."
RL Comp. Biochem. Physiol. C, Pharmacol. Toxicol. Endocrinol. 110:297-
RL 304(1995).
SQ SEQUENCE 8 AA; 989 MW; 954772CAA87B0B59 CRC64;

Query Match 48.0%; Score 12; DB 5; Length 8;
Best Local Similarity 14.3%; Pred. No. 1e+06;
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7
DB 2 YEGDVY 8

RESULT 13
ID Q34909 PRELIMINARY; PRT; 8 AA.
AC Q34909;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
OS Locusta migratoria (Migratory locust).
OS Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxId=7004;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88223478; PubMed=2836084;
RA McCracken A., Uhlenbusch I., Gellissen G.;
RT "Structure of the cloned locusta migratoria mitochondrial genome:
RT restriction mapping and sequence of its ND-1 (URR-1) gene.";
RL Curr. Genet. 11:625-630(1987).
DR EMBL; X05286; CAA28905.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match 48.0%; Score 12; DB 8; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 7
DB 4 IXLKH 8

RESULT 14
ID Q37854 PRELIMINARY; PRT; 8 AA.
AC Q37854;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Coliphage gene of unknown function, S' end (Fragment).
OS Bacteriophage R17.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Leviviruses.
OX NCBI_TaxId=12026;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=73224987; PubMed=4352721;  
 RA Rensing U.F.E.;  
 RT "A sequence of seventy-three nucleotides from the Colipage R17  
 genome."  
 RL Biochem. J. 131:593-604(1973).  
 DR EMBL: M24820; AAA72755.1; -.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 969 MW; ECB45412C1E72726 CRC64;  
 Query Match 48.0%; Score 12; DB 9; Length 8;  
 Best Local Similarity 20.0%; Pred. No. 1e+06;  
 Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 XXVXL 8  
 DB 1 MLTAV 5  
 RESULT 15  
 ID P87488 PRELIMINARY; PRT; 8 AA.  
 AC P87488;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Growth hormone 2 (Fragment).  
 GN GH-2-A OR GH-2-B.  
 OS Oncorhynchus kisutch (Coho salmon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Procarangopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8019;  
 RN [1]  
 RP SEQUENCE OF 41-48 FROM N.A.  
 RX MEDLINE=94173883; PubMed=8127856;  
 RA Forbes S.H.; Knudsen K.L.; North T.W.; Allendorf F.W.;  
 RT "One of two growth hormone genes in coho salmon is sex-linked."  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:0-0(0).  
 DR EMBL: U04930; AAD13472.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 902 MW; 92233732D5A5B326 CRC64;  
 Query Match 48.0%; Score 12; DB 13; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1e+06;  
 Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 XQXVXHL 8  
 DB 1 QKSSVLKL 8  
 RESULT 16  
 ID P82082 PRELIMINARY; PRT; 8 AA.  
 AC P82082;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE DYNASTIN 4.  
 OS Limnodynastes salmuni (Salmuni 8-striped frog).  
 OC Amphibia; Batrachia; Chordata; Vertebrata; Euteleostomi;  
 OC Limnodynastinae; Limnodynastes.  
 OX NCBI\_TaxID=39404;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RT TISSUE=SKIN SECRETION;

RA Bradford A.M.; Raftery M.J.; Bowie J.H.; Wallace J.C.; Tyler M.J.;  
 RT "Peptides from Australian frogs. The structure of the dynastins from  
 RT Limnodynastes salmuni and Fletcherin from Limnodynastes fletcheri."  
 RL Aust. J. Chem. 46:1235-1244(1993).  
 CC -1- MASS SPECTROMETRY; MW=772; METHOD=FAE.  
 SQ SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;  
 Query Match 48.0%; Score 12; DB 13; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1e+06;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 XXVXL 8  
 DB 1 GLVSNL 6  
 RESULT 17  
 ID Q15894 PRELIMINARY; PRT; 8 AA.  
 AC Q15894;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE (Clone XP587B) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lee C.-C.; Yazdani A.; Wehnert M.; Bailey J.; Couch L.; Xiong M.;  
 RA Coolbaugh M.I.; Chinault C.A.; Baldini A.; Lindsay E.A.; Zhao Z.-Y.;  
 RA Caskey C.T.H.;  
 RT "Isolation of chromosome-specific genes by reciprocal probing of  
 RT arrayed cDNAs and cosmid libraries."  
 RL Hum. Mol. Genet. 0:0-0(1995).  
 DR EMBL: L32074; AAA73884.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 952 MW; BEC735B1E1F1B6D6 CRC64;  
 Query Match 44.0%; Score 11; DB 4; Length 8;  
 Best Local Similarity 20.0%; Pred. No. 1e+06;  
 Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 XXVXH 7  
 DB 1 MOTHN 5  
 RESULT 18  
 ID Q9UD24 PRELIMINARY; PRT; 8 AA.  
 AC Q9UD24;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE RHD protein (Fragment).  
 GN RHD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97260406; PubMed=9106526;  
 RA Matsui G.; Cherif-Zahar B.; Mouru I.; Cartton J.P.;  
 RT "Characterization of the recombination hot spot involved in the  
 RT genomic rearrangement leading to the hybrid D-Ce-D gene in the DVI  
 phenotype."  
 RL Am. J. Hum. Genet. 60:808-817(1997).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=93066356; PubMed=1438298;  
 RA Le Van Kim C., Mourou I., Cherif-Zahar B., Raynal V., Cherrier C.,  
 RT "Molecular cloning and primary structure of the human blood group Rh  
 polyepitope."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10925-10929(1992).  
 DR EMBL; Z97031; CAB09727.1; -.  
 GO GO:0016021; C:integral to membrane; NAS.  
 FT NON TER 1 1  
 SQ SEQUENCE 8 AA; 1042 MW; D296944691FBSAB1 CRC64;  
 Query Match 44.0%; Score 11; DB 4; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1e+06;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHL 8  
 Db 3 YHM 5  
 RESULT 19  
 Q9UMH9 PRELIMINARY; PRT; 8 AA.  
 ID Q9UMH9  
 AC Q9UMH9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE RHCE protein (Fragment).  
 GN RHCE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=97260406; PubMed=9106526;  
 RA Matsasi G., Cherif-Zahar B., Mourou I., Carttron J.P.,  
 RT "Characterization of the recombination hot spot involved in the  
 genomic rearrangement leading to the hybrid D-CE-D gene in the DVI  
 phenotype."  
 RL Am. J. Hum. Genet. 60:808-817(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=90349591; PubMed=1696722;  
 RA Cherif-Zahar B., Bloy C., Le Van Kim C., Blanchard D., Bailly P.,  
 RA Hernand P., Salmon C., Carttron J.-P., Colin Y.,  
 RT "Molecular cloning and protein structure of a human blood group Rh  
 polypeptide."  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6243-6247(1990).  
 DR EMBL; Z97030; CAB09726.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 8 AA; 1049 MW; C007244691FBSAB1 CRC64;  
 Query Match 44.0%; Score 11; DB 4; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1e+06;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 XHL 8  
 Db 3 YHM 5  
 RESULT 20  
 O15899 PRELIMINARY; PRT; 8 AA.  
 AC O15899;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE 12D3 antigen (Fragment).  
 GN B012D3.  
 OS Babesia ovis.  
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesidae; Babesia.  
 OX NCBI\_TaxID=5869;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Ankara;  
 RA Silins G.U., Blakeley R.L., Riddles P.W.;  
 RT "Characterization of the transcriptional control region of the 12D3  
 antigen gene from the sporozoan Babesia ovis."  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBD databases.  
 DR EMBL; U44919; AAB6365.1; -.  
 FT NON TER 8 8  
 SQ SEQUENCE 8 AA; 992 MW; F0C7273411B2C726 CRC64;

QY 3 XXVXHL 8  
 Db 1 MLVTRL 6  
 Query Match 44.0%; Score 11; DB 5; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1e+06;  
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 RESULT 21  
 P79940 PRELIMINARY; PRT; 8 AA.  
 ID P79940  
 AC P79940;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Xmei1-4 protein (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=97202105; PubMed=9049632;  
 RX Steelman S., Moskow J.J., Muzynski K., North C., Druck T.,  
 RA Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.;  
 RT "Identification of a conserved family of Meis1-related homeobox  
 RT genes."  
 RL Genome Res. 7:142-156(1997).  
 DR EMBL; U68389; AAB19199.1; -.  
 FT TRANSFAC; T03410; -.  
 SQ SEQUENCE 8 AA; 1187 MW; 278B51F37B1F40B CRC64;

QY 2 OXXVXH 7  
 Db 1 ERHWH 6  
 Query Match 44.0%; Score 11; DB 13; Length 8;  
 Best Local Similarity 16.7%; Pred. No. 1e+06;  
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 RESULT 22  
 P82083 PRELIMINARY; PRT; 8 AA.  
 ID P82083  
 AC P82083;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE DYNASTIN 5.  
 OS Limnodynastes salmiani (Salmian's-a-striped frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
OX NCBI_TaxID=39404;
RN (1)
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastins from
RT Limnodynastes salmiani and Fletcherin from Limnodynastes fletcheri.";
RL Aust. J. Chem. 46:1235-1244(1993)
CC -1- MASS SPECTROMETRY: MW=786; METHOD=PAB.
SQ SEQUENCE 8 AA; 786 MW; 7858772455B05728 CRC64;

Query Match 44.0%; Score 11; DB 13; Length 8;
Best Local Similarity 16.7%; Pred. No. 1e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHL 8
DB 1 GLISNL 6

RESULT 23
Q45615 PRELIMINARY; PRT; 8 AA.
ID Q45615;
AC Q45615;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GucB protein (Fragment).
GN GUTB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=94253000; Pubmed=8195086;
RA Ye R., Wong S.L.;
RT "Transcriptional regulation of the Bacillus subtilis glucitol
RT dehydrogenase gene.";
RL J. Bacteriol. 176:3314-3320(1994).
DR EMBL; L16626; AAA20875.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 927 MW; FD56C772D1A1F1A6 CRC64;

Query Match 40.0%; Score 10; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VXH 7
DB 1 MTH 3

RESULT 24
P77556 PRELIMINARY; PRT; 8 AA.
ID P77556;
AC P77556;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE TRAY (Fragment).
GN TRAY.
OS Escherichia coli.
OC Plasmid incFII R1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ECOR11;
RX MEDLINE=96400908; Pubmed=8807284;

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RA Boyd E.F., Hill C.W., Rich S.M., Hartl D.L.;
RT "Mosaic structure of plasmids from natural populations of Escherichia
RT coli.";
RL Genetics 143:1091-1100(1996).
DR EMBL; U50661; AAC44245.1; -.
DR EMBL; U50650; AAC44234.1; -.
DR EMBL; U50651; AAC44235.1; -.
DR EMBL; U50652; AAC44236.1; -.
DR EMBL; U50653; AAC44237.1; -.
DR EMBL; U50654; AAC44238.1; -.
DR EMBL; U50655; AAC44239.1; -.
DR EMBL; U50656; AAC44240.1; -.
DR EMBL; U50657; AAC44241.1; -.
DR EMBL; U50658; AAC44242.1; -.
DR EMBL; U50659; AAC44243.1; -.
DR EMBL; U50660; AAC44244.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON TER 1
SQ SEQUENCE 8 AA; 834 MW; D35A5B0544735A1 CRC64;

Query Match 40.0%; Score 10; DB 2; Length 8;
Best Local Similarity 12.5%; Pred. No. 1e+06;
Matches 1; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 XOXVXHL 8
DB 1 TSINISL 8

RESULT 25
Q93SP2 PRELIMINARY; PRT; 8 AA.
ID Q93SP2;
AC Q93SP2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Quaternary ammonium compound-resistance protein Qacdelta1
DE (Fragment).
GN QACDELTA1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=YMC704; TRANSPOSON=class I integron;
RA Lee K., Chong Y., Yum J.H., Yong D., Livermore D.M.;
RT "YIM-2 metallo-beta-lactamase gene-containing integron in a
RT Pseudomonas aeruginosa clinical isolate.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029772; AA050441.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 920 MW; FE2729C732C87336 CRC64;

Query Match 40.0%; Score 10; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXHL 8
DB 2 KGVLF 7

RESULT 26
Q8GL21 PRELIMINARY; PRT; 8 AA.
ID Q8GL21;
AC Q8GL21;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.

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OS Borrelia burgdorferi (Lyme disease spirochete).
OC Plasmid group cp32-8.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SH-2-82;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi exp genes and their cp32
RT prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142094; AAN17903.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON TER
SQ SEQUENCE 8 AA; 1042 MW; 143724437204373 CRC64;

Query Match          40.0%; Score 10; DB 2; Length 8;
Best Local Similarity 14.3%; Pred. No. 1e+06;
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 OXXVXH 8
DB 1 KWILKNL 7

RESULT 27
ID 013591 PRELIMINARY; PRT; 8 AA.
AC 013591;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE ORP YNL337W (Fragment).
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycaceae.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Obermayer B., Piravandi E., Rinke M.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z71612; CAA96271.2; -.
FT NON TER
SQ SEQUENCE 8 AA; 1005 MW; 5CA441E449C9C720 CRC64;

Query Match          40.0%; Score 10; DB 3; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
DB 2 LFFNH 6

RESULT 28
ID 09BYYS PRELIMINARY; PRT; 8 AA.
AC 09BYYS;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618 (2001).
DR EMBL; AY011664; AAG47575.1; -.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003677; F:DNA binding; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
FT NON TER
SQ SEQUENCE 8 AA; 1006 MW; DF02C331ERAB572A CRC64;

Query Match          40.0%; Score 10; DB 4; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
DB 1 DLYCH 5

RESULT 29
ID 015893 PRELIMINARY; PRT; 8 AA.
AC 015893;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE (Clone XP587N) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinnault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0 (1995).
DR EMBL; I32073; AAA73883.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 874 MW; DAA1BD7376456C5 CRC64;

Query Match          40.0%; Score 10; DB 4; Length 8;
Best Local Similarity 16.7%; Pred. No. 1e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXVXH 6
DB 1 SQNPLO 6

RESULT 30
ID 081UB8 PRELIMINARY; PRT; 8 AA.
AC 081UB8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CD95 antigen (Fragment).
GN CD95.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22404279; Pubmed=12516573;

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RA Kurth J., Pernio A., Schmitz R., Iking-Konert C., Chiorazzi N.,
RA Thompson K.M., Winkler T., Rajewsky K., Kuipers R.;
RT "Lack of deleterious somatic mutations in the CD95 gene of
RT plasmablasts from systemic lupus erythematosus patients and
RT autotibody-producing cell lines."
RL Eur. J. Immunol. 32:3785-3792(2002).
DR EMBL, AJ509178; CAD48928.1; -.
FT NON_TER
FT SEQUENCE 8 AA; 846 MW; 34B724405DC2D1AB CRC64;
SQ
Query Match 40.0%; Score 10; DB 4; Length 8;
Best Local Similarity 14.3%; Pred. No. 1e+06;
Matches 1; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 2 QXXVXH 8
DB 1 ETVAIHL 7
RESULT 31
Q8MUN6 PRELIMINARY; PRT; 8 AA.
AC Q8MUN6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN MPI.
OS Heliconius melpomene melpomene.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.
OC NCBI_TaxID=171917;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STRI-B-441-Mpi-2;
RA Bull V., Beltran M., Berningham E., Jiggins C., McMillan O.,
RA Mallet J.;
RT "Molecular evidence for gene flow between species of Heliconius.";
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF516247; AAM61933.1; -.
DR GO: GO:0016553; P: isomerase activity; IEA.
KW isomerase.
FT NON_TER
FT NON_TER
FT SEQUENCE 8 AA; 977 MW; 16E736DB1DD1EAA3 CRC64;
SQ
Query Match 40.0%; Score 10; DB 5; Length 8;
Best Local Similarity 14.3%; Pred. No. 1e+06;
Matches 1; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 XQXXVXH 7
DB 2 DHAEQLH 8
RESULT 32
Q02032 PRELIMINARY; PRT; 8 AA.
AC Q02032;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Metallothionein (Fragment).
GN LPM12.
OS Lytechinus pictus (Painted sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Lytechinus.
OC NCBI_TaxID=7653;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=97264487; PubMed=9110313;
RA Cserjesi P., Fang H., Brandhorst B.P.;
RT "Metallothionein gene expression in embryos of the sea urchin
RT Lytechinus pictus."
RL Mol. Reprod. Dev. 47:39-46(1997).
DR EMBL, U83400; AAB58320.1; -.
FT NON_TER
FT SEQUENCE 8 AA; 823 MW; EBD5A2C1F7686766 CRC64;
SQ
Query Match 40.0%; Score 10; DB 5; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 6 XHL 8
DB 4 PHV 6
RESULT 33
Q86BS9 PRELIMINARY; PRT; 8 AA.
AC Q86BS9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cyclin B (Fragment).
GN Cyclin B.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Strongylocentrotidae;
OC Strongylocentrotus.
OC NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96027756; PubMed=7546293;
RA Thatcher J.D., McBride B., Katula K.S.;
RT "Promoter binding factors regulating cyclin B transcription in the sea
RT urchin embryo."
RL DNA Cell Biol. 14:869-881(1995).
DR EMBL, S80441; AAP32224.1; -.
KW Cyclin.
FT NON_TER
FT SEQUENCE 8 AA; 897 MW; EE645411ADD1EDD6 CRC64;
SQ
Query Match 40.0%; Score 10; DB 5; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 VXH 7
DB 1 MAH 3
RESULT 34
Q9TT78 PRELIMINARY; PRT; 8 AA.
AC Q9TT78;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Thymidylate synthase (Fragment).
GN TS.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015404; PubMed=1130975;
RA Brouillette J.A., Andrew J.R., Vemta P.J.;
RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
RT method."
RL Mamm. Genome 11:1079-1086(2000).

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DR EMBL; AF202073; AAF20918.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 899 MW; 6731A1E059CA867 CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 6; Length 8;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 2 GDFIH 6

RESULT 35
Q9BF82 PRELIMINARY; PRT; 8 AA.
AC Q9BF82;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Ursus arctos (Brown bear) (Grizzly bear).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=9644;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011683; AAG47591.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 6; Length 8;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 36
Q9BFC2 PRELIMINARY; PRT; 8 AA.
AC Q9BFC2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011621; AAG47536.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 6; Length 8;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 37
Q9BF90 PRELIMINARY; PRT; 8 AA.
AC Q9BF90;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Tragelaphus eurycerus (Bongo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Tragelaphus.
OX NCBI_TaxID=69297;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011673; AAG47583.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 6; Length 8;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 38
Q9BFB1 PRELIMINARY; PRT; 8 AA.
AC Q9BFB1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Echinos telfairi (lesser hedgehog tenrec).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Echinos.
OX NCBI_TaxID=9371;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011632; AAG47547.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EAB572A CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 6; Length 8;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5
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RESULT 39
Q9BFA1 ID Q9BFA1 PRELIMINARY; PRT; 8 AA.
AC Q9BFA1;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Ateles fusciceps (Brown-headed spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles.
OX NCBI_TaxID=9508;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011660; AAC47571.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 40
Q9BF87 ID Q9BF87 PRELIMINARY; PRT; 8 AA.
AC Q9BF87;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Tapirus indicus (Asiatic tapir) (Malayan tapir).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perisodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID=9802;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011678; AAC47586.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 41
Q9BFB9 ID Q9BFB9 PRELIMINARY; PRT; 8 AA.
AC Q9BFB9;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)

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DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Euphractus sexinctus (Six-banded armadillo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Dasypodidae; Euphractus.
OX NCBI_TaxID=143300;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011624; AAC47539.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 42
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AC Q9BFB8;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Chaetophactus villosus (South American armadillo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Dasypodidae; Chaetophactus.
OX NCBI_TaxID=29080;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; Pubmed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011625; AAC47540.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EBAB572A CRC64;

Query Match 40.0%; Score 10; DB 6; Length 8;
Best Local Similarity 20.0%; Pred. No. 1e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 XXVXH 7
Db 1 DLYCH 5

RESULT 43
Q9BFA0 ID Q9BFA0 PRELIMINARY; PRT; 8 AA.
AC Q9BFA0;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.

```

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OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011631; AAC47572.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 1006 MW; DF02C31IEAB572A CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 6; Length 8;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 3 XXVXH 7
DB 1 DLVCH 5

RESULT 44
O9BFA8 PRELIMINARY; PRT; 8 AA.
AC O9BFA8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
OS CREM.
OS Loxodonta africana (African elephant).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Loxodonta.
OX NCBI_TaxID=9785;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011635; AAC47550.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 978 MW; DF1DD33IEAB572A CRC64;

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Query Match
Best Local Similarity 40.0%; Score 10; DB 6; Length 8;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 3 XXVXH 7
DB 1 DLVCH 5

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RESULT 45
O9BFA9 PRELIMINARY; PRT; 8 AA.
AC O9BFA9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
OS CREM.
OS Procavia capensis (Cape hyrax) (Rock dassie).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Hyracoidea; Procaviidae; Procavia.
OX NCBI_TaxID=9813;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RT "Molecular phylogenetics and the origins of placental mammals.";

```

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RL Nature 409:614-618(2001).
DR EMBL; AY011634; AAC47549.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 978 MW; DF1DD33IEAB572A CRC64;

Query Match
Best Local Similarity 40.0%; Score 10; DB 6; Length 8;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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```

QY 3 XXVXH 7
DB 1 DLVCH 5

Search completed: August 19, 2004, 15:50:49
Job time : 32 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using SW model

Run on: August 19, 2004, 15:47:57 ; Search time 13.5 Seconds  
(without alignments)  
30.593 Million cell updates/sec

Title: VARIANT2  
Perfect score: 25  
Sequence: 1 XQXXVXHI 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues  
Total number of hits satisfying chosen parameters: 13858

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	25	100.0	8 4 US-09-248-381-18	Sequence 18, Appl
2	25	100.0	8 4 US-09-248-381-19	Sequence 19, Appl
3	23	92.0	8 1 US-08-168-390-11	Sequence 11, Appl
4	23	92.0	8 1 US-08-168-390-12	Sequence 12, Appl
5	23	92.0	8 2 US-08-337-127-9	Sequence 9, Appl
6	23	92.0	8 4 US-09-260-846-9	Sequence 9, Appl
7	23	92.0	8 4 US-09-248-381-16	Sequence 16, Appl
8	23	92.0	8 4 US-09-248-381-17	Sequence 17, Appl
9	23	92.0	8 6 5217955-32	Patent No. 5217955
10	23	92.0	8 6 5217955-34	Patent No. 5217955
11	23	92.0	8 6 5217955-35	Patent No. 5217955
12	23	92.0	8 6 5217955-36	Patent No. 5217955
13	23	92.0	8 1 US-08-031-325A-27	Sequence 27, Appl
14	21	84.0	8 2 US-08-337-127-4	Sequence 4, Appl
15	21	84.0	8 2 US-08-337-127-8	Sequence 8, Appl
16	21	84.0	8 4 US-09-260-846-4	Sequence 4, Appl
17	21	84.0	8 4 US-09-260-846-8	Sequence 8, Appl
18	21	84.0	8 4 US-09-260-846-8	Sequence 8, Appl
19	21	84.0	8 6 5217955-31	Patent No. 5217955
20	21	84.0	8 6 5217955-33	Patent No. 5217955
21	21	84.0	8 6 5217955-38	Patent No. 5217955
22	20	80.0	8 3 US-08-444-818-632	Sequence 632, App
23	20	80.0	8 6 5217955-37	Patent No. 5217955
24	19	76.0	8 3 US-08-444-818-633	Sequence 633, App
25	18	72.0	8 1 US-08-168-390-13	Sequence 13, Appl
26	18	72.0	8 1 US-08-168-390-14	Sequence 14, Appl
27	18	72.0	8 1 US-08-178-268-16	Sequence 16, Appl

28	18	72.0	8 3 US-09-082-279B-1459	Sequence 1459, Ap
29	18	72.0	8 4 US-09-315-304B-1612	Sequence 1612, Ap
30	18	72.0	8 4 US-09-834-784-1459	Sequence 1459, Ap
31	18	72.0	8 4 US-09-350-641C-1613	Sequence 1613, Ap
32	17	68.0	8 1 US-08-387-634-3	Sequence 3, Appl
33	17	68.0	8 3 US-08-816-346-20	Sequence 20, Appl
34	17	68.0	8 4 US-09-335-111-20	Sequence 10, Appl
35	17	68.0	8 3 US-09-515-965A-1846	Sequence 1846, Ap
36	17	68.0	8 6 5217955-25	Patent No. 5217955
37	17	68.0	8 6 5217955-27	Patent No. 5217955
38	17	68.0	8 6 5217955-28	Patent No. 5217955
39	16	64.0	8 1 US-08-457-804-5	Sequence 5, Appl
40	16	64.0	8 1 US-08-843-035-16	Sequence 16, Appl
41	16	64.0	8 1 US-08-178-268-10	Sequence 10, Appl
42	16	64.0	8 2 US-07-885-089B-25	Sequence 25, Appl
43	16	64.0	8 2 US-08-755-496A-16	Sequence 16, Appl
44	16	64.0	8 3 US-08-925-002-37	Sequence 37, Appl
45	16	64.0	8 3 US-08-444-818-432	Sequence 432, App

## ALIGNMENTS

```

RESULT 1
US-09-248-381-18
; Sequence 18, Application US/09248381
; Patent No. 6492330
; GENERAL INFORMATION:
; APPLICANT: MUKHERJEE, RAMA
; APPLICANT: JAGGI, MANU
; APPLICANT: PRASAD, SUDHANAND
; APPLICANT: BURMAN, ANAND C
; APPLICANT: RAJENDRAN, PRAVEEN
; APPLICANT: MATHER, ARCHANA
; APPLICANT: SINGH, ANU T
; TITLE OF INVENTION: ANTICARCINOGENIC DRUGS
; FILE REFERENCE: U 011695-8
; CURRENT APPLICATION NUMBER: US/09/248,381
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This peptide
; OTHER INFORMATION: was synthetically generated.
; FEATURE:
; NAME/KEY: MOD_RBS
; LOCATION: (1)
; OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Alb
; US-09-248-381-18

Query Match      100.0%; Score 25; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. NO. 3e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 XQXXVXHI 8
Db      1 XQXXVXHI 8

RESULT 2
US-09-248-381-19
; Sequence 19, Application US/09248391
; Patent No. 6492330
; GENERAL INFORMATION:
; APPLICANT: MUKHERJEE, RAMA

```

```
/ APPLICANT: JAGGI, MANU
/ APPLICANT: PRASAD, SUDHANAND
/ APPLICANT: BURMAN, ANAND C
/ APPLICANT: RAJENDRAN, PRAVEEN
/ APPLICANT: MATHEUR, ARCHANA
/ APPLICANT: SINGH, ANU T
/ TITLE OF INVENTION: ANTIANGIOGENIC DRUGS
/ FILE REFERENCE: U 011695-8
/ CURRENT APPLICATION NUMBER: US/09/248,381
/ CURRENT FILING DATE: 1999-02-11
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: This peptide
/ OTHER INFORMATION: was synthetically generated.
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)_
/ OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe
/ NAME/KEY: MOD_RES
/ LOCATION: (6)
/ OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Alb
/ US-09-248-381-19
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Query Match          100.0%; Score 25; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 XQXVXHI 8
        ||:||||
Db      1 XQWAVXHI 8
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RESULT 3
/ US-08-168-390-11
/ Sequence 11, Application US/08168390
/ Patent No. 5620955
/ GENERAL INFORMATION:
/ APPLICANT: Knight, Martha
/ APPLICANT: Takahashi, Kazayuki
/ APPLICANT: Chandrasekhar, Bhaskar
/ TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sterne, Kessler, Goldstein & Fox
/ STREET: 1100 New York Avenue, Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/168,390
/ FILING DATE: Herewith
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Goldstein, Jorge A.
/ REGISTRATION NUMBER: 29,021
/ REFERENCE/DOCKET NUMBER: 0871.0040001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540
/ TELEX: 248636 SSK
/ OTHER INFORMATION: FOR SEQ ID NO: 11:
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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 1
/ OTHER INFORMATION: /note="The amino-terminal residue
/ OTHER INFORMATION: comprises one of several chemical end caps."
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 8
/ OTHER INFORMATION: /note="The carboxy-terminal
/ OTHER INFORMATION: residue comprises an ethyl ester."
/ US-08-168-390-11
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Query Match          92.0%; Score 23; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 XQXVXHI 8
        ||:||||
Db      1 XQWAVGHL 8
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RESULT 4
/ US-08-168-390-12
/ Sequence 12, Application US/08168390
/ Patent No. 5620955
/ GENERAL INFORMATION:
/ APPLICANT: Knight, Martha
/ APPLICANT: Takahashi, Kazayuki
/ APPLICANT: Chandrasekhar, Bhaskar
/ TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sterne, Kessler, Goldstein & Fox
/ STREET: 1100 New York Avenue, Suite 600
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/168,390
/ FILING DATE: Herewith
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Goldstein, Jorge A.
/ REGISTRATION NUMBER: 29,021
/ REFERENCE/DOCKET NUMBER: 0871.0040001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540
/ TELEX: 248636 SSK
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 1
/ OTHER INFORMATION: /note="The amino-terminal residue
/ OTHER INFORMATION: comprises one of several chemical end caps."
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 6
/ OTHER INFORMATION: /note="The alanine at position 6
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; OTHER INFORMATION: 1s dextrorotatory alanine."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note="The carboxy-terminal
; OTHER INFORMATION: residue comprises an ethyl ester."
US-08-168-390-12

Query Match          92.0%; Score 23; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 XQXXVXHI 8
       :|::|::|:
Db      1 EQWAVGHL 8

RESULT 5
US-08-337-127-9
; Sequence 9, Application US/08337127
; Patent No. 5877277
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun H.
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,127
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/779,039
; FILING DATE: 10/18/91
; APPLICATION NUMBER: 07/502,438
; FILING DATE: 03/30/90
; APPLICATION NUMBER: 07/397,169
; FILING DATE: 08/21/89
; APPLICATION NUMBER: 07/376,555
; FILING DATE: 07/07/89
; APPLICATION NUMBER: 07/317,941
; FILING DATE: 03/02/89
; APPLICATION NUMBER: 07/282,328
; FILING DATE: 12/09/88
; APPLICATION NUMBER: 07/257,998
; FILING DATE: 10/14/88
; APPLICATION NUMBER: 07/248,771
; FILING DATE: 09/23/88
; APPLICATION NUMBER: 07/207,759
; FILING DATE: 06/16/88
; APPLICATION NUMBER: 07/204,171
; FILING DATE: 06/08/88
; APPLICATION NUMBER: 07/173,311
; FILING DATE: 03/25/88
; APPLICATION NUMBER: 07/100,571
; FILING DATE: 09/24/87
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00537/009000

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The sequence contains at
; OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,
; OTHER INFORMATION: and has an methyl ester C-terminus (i.e., COOCH3),
; OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., COOH).
US-08-337-127-9

Query Match          92.0%; Score 23; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 XQXXVXHI 8
       :|::|::|:
Db      1 EQWAVGHL 8

RESULT 6
US-09-260-846-9
; Sequence 9, Application US/09260846
; Patent No. 6307017
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun Hyuk
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
; FILE REFERENCE: 00537/009000
; CURRENT APPLICATION NUMBER: US/09/260,846
; CURRENT FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
; NAME/KEY: MOD_RBS
; LOCATION: (1)-
; OTHER INFORMATION: pyroglutamate
; FEATURE:
; OTHER INFORMATION: this peptide has a methyl ester C-terminus
US-09-260-846-9

Query Match          92.0%; Score 23; DB 4; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 XQXXVXHI 8
       :|::|::|:
Db      1 EQWAVGHL 8

RESULT 7
US-09-248-381-16
; Sequence 16, Application US/09248381
; Patent No. 6492330
; GENERAL INFORMATION:
; APPLICANT: MUKHERJEE, RAMA
; APPLICANT: JAGGI, MANU
; APPLICANT: PRASAD, SUDHANAND
; APPLICANT: BURMAN, ANAND C
; APPLICANT: RAJENDRAN, PRAVEEN
```

```
APPLICANT: MATHUR, ARCHANA
APPLICANT: SINGH, ANU T
TITLE OF INVENTION: ANTITUMORIGENIC DRUGS
FILE REFERENCE: U 011695-8
CURRENT APPLICATION NUMBER: US/09/248,381
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: This peptide
OTHER INFORMATION: was synthetically generated.
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)_RES
OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe;
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)_RES
OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Alb
US-09-248-381-16
```

```
Query Match          92.0%; Score 23; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 XQXXVXHI 8
DB 1 XQXVGHIL 8
```

```
RESULT 8
US-09-248-381-17
Sequence 17, Application US/09248381
Patent No. 6492330
GENERAL INFORMATION:
APPLICANT: MUGHERJEE, RAMA
APPLICANT: JAGGI, MANU
APPLICANT: PRASAD, SUDHANAND
APPLICANT: BURMAN, ANAND C
APPLICANT: RAJENDRAN, PRAVEEN
APPLICANT: MATHUR, ARCHANA
APPLICANT: SINGH, ANU T
TITLE OF INVENTION: ANTITUMORIGENIC DRUGS
FILE REFERENCE: U 011695-8
CURRENT APPLICATION NUMBER: US/09/248,381
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: This peptide
OTHER INFORMATION: was synthetically generated.
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)_RES
OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe
NAME/KEY: MOD_RES
LOCATION: (6)_RES
OTHER INFORMATION: /product=2-amino-isobutyric acid/label=Alb
US-09-248-381-17
```

```
Query Match          92.0%; Score 23; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 XQXXVXHI 8
DB 1 XQXVGHIL 8
```

```
RESULT 9
5217955-32
Patent No. 5217955
APPLICANT: ABOGDE, ARTHUR E.;MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 440,039
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 408,125
FILING DATE: 15-SEP-1989
SEQ ID NO:32
LENGTH: 8
5217955-32
```

```
Query Match          92.0%; Score 23; DB 6; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 XQXXVXHI 8
DB 1 FQWAVGHL 8
```

```
RESULT 10
5217955-34
Patent No. 5217955
APPLICANT: ABOGDE, ARTHUR E.;MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 440,039
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 408,125
FILING DATE: 15-SEP-1989
SEQ ID NO:34
LENGTH: 8
5217955-34
```

```
Query Match          92.0%; Score 23; DB 6; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 XQXXVXHI 8
DB 1 XQXVGHIL 8
```

```
RESULT 11
5217955-35
Patent No. 5217955
APPLICANT: ABOGDE, ARTHUR E.;MOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225
FILING DATE: 09-MAY-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 440,039
```



FILING DATE: 21-NOV-1989  
 APPLICATION NUMBER: 408,125  
 FILING DATE: 15-SEP-1989  
 SEQ ID NO:35:  
 LENGTH: 8  
 5217955-35

Query Match 92.0%; Score 23; DB 6; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 3e+05;  
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 XQXXVXH 8  
 Db 1 XQWAVAH 8

RESULT 12  
 5217955-36  
 Patent No. 5217955  
 APPLICANT: ABOGDEEN, ARTHUR E.; MOREAU, JACQUES-PIERRE  
 TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
 OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN  
 NUMBER OF SEQUENCES: 42  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/520,225  
 FILING DATE: 09-MAY-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 440,039  
 FILING DATE: 21-NOV-1989  
 APPLICATION NUMBER: 408,125  
 FILING DATE: 15-SEP-1989  
 SEQ ID NO:36:  
 LENGTH: 8  
 5217955-36

Query Match 92.0%; Score 23; DB 6; Length 8;  
 Best Local Similarity 37.5%; Pred. No. 3e+05;  
 Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 XQXXVXH 8  
 Db 1 FQWAVAH 8

RESULT 13  
 US-08-031-325A-27  
 Sequence 27, Application US/08031325A  
 Patent No. 5369094  
 GENERAL INFORMATION:  
 APPLICANT: Schally, Andrew V.  
 APPLICANT: Cai, Renzh  
 TITLE OF INVENTION: POLYPEPTIDE BOMBESIN ANTAGONISTS  
 NUMBER OF SEQUENCES: 37  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: OMRI M. BEHR, ESQ  
 STREET: 325 PIERSON AVENUE  
 CITY: EDISON  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 08837  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/031,325A  
 FILING DATE: 15-MAR-1993  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/619,747  
 FILING DATE: 29-NOV-1990  
 ATTORNEY/AGENT INFORMATION:

NAME: BEHR, OMRI M.  
 REGISTRATION NUMBER: 22,940  
 REFERENCE/DOCKET NUMBER: SHAL3-0-014  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 494-5240  
 TELEFAX: (908) 494-0428  
 TELEX: 511642 BEPATEDIN  
 INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1  
 OTHER INFORMATION: /note= "Res 1 = (R1) (R2)-A0-A1, where A0  
 OTHER INFORMATION: = deleted; A1 = D-Phe, D-Tyr or D-Nal; R1 and R2 = H"

NAME/KEY: misc\_feature

LOCATION: 8  
 OTHER INFORMATION: /note= "Res 8 = A8-N, where N = -N(R8)-  
 OTHER INFORMATION: CH(Z1)-R4-CH(Z2)-CO-V, where R4 = CH2NH; Z1 = -CH2CH(CH3)2; Z2  
 OTHER INFORMATION: H or  
 OTHER INFORMATION: COEL, where E1 = Cl-20 alkyl"

US-08-031-325A-27  
 Query Match 84.0%; Score 21; DB 1; Length 8;  
 Best Local Similarity 57.1%; Pred. No. 3e+05;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 XQXXVXH 7  
 Db 1 XQWAVGH 7

RESULT 14  
 US-08-337-127-4  
 Sequence 4, Application US/08337127  
 Patent No. 5877277  
 GENERAL INFORMATION:  
 APPLICANT: Coy, David H.  
 APPLICANT: Moreau, Jacques-Pierre  
 APPLICANT: Kim, Sun H.  
 TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN  
 TITLE OF INVENTION: ANALOGS  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 COMPUTER: IBM PS/2 Model 502 or 55SX  
 OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
 SOFTWARE: Nordperfect (Version 5.0)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/337,127  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/779,039  
 FILING DATE: 10/18/91  
 APPLICATION NUMBER: 07/502,438  
 FILING DATE: 03/30/90  
 APPLICATION NUMBER: 07/397,169  
 FILING DATE: 08/21/89  
 APPLICATION NUMBER: 07/376,555

```
;
; APPLICATION NUMBER: 07/07/89
; FILING DATE: 07/317,941
; APPLICATION NUMBER: 03/02/89
; FILING DATE: 07/282,328
; APPLICATION NUMBER: 12/09/88
; FILING DATE: 07/257,998
; APPLICATION NUMBER: 10/14/88
; FILING DATE: 07/248,771
; APPLICATION NUMBER: 09/23/88
; FILING DATE: 07/207,759
; APPLICATION NUMBER: 06/16/88
; FILING DATE: 07/204,171
; APPLICATION NUMBER: 06/08/88
; FILING DATE: 07/173,311
; APPLICATION NUMBER: 03/25/88
; FILING DATE: 07/100,571
; APPLICATION NUMBER: 09/24/87
; FILING DATE: 07/100,571
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00537/00900D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The sequence contains at
; OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,
; OTHER INFORMATION: and has an amide C-terminus (i.e., COYNH2), rather
; OTHER INFORMATION: than a carboxyl C-terminus (i.e., COYOH). Xaa stands for
; OTHER INFORMATION: statine.
; US-08-337-127-4
;
; Query Match
; Best Local Similarity 84.0%; Score 21; DB 2; Length 8;
; Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 XQXXVXH 7
; Db 1 EQWAVGH 7
;
; RESULT 15
; US-08-337-127-8
; Sequence 8, Application US/08337127
; Patent No. 5877277
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun H.
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 555X
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
```

```
;
; APPLICATION NUMBER: US/08/337,127
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/779,039
; FILING DATE: 10/18/91
; APPLICATION NUMBER: 07/502,438
; FILING DATE: 03/30/90
; APPLICATION NUMBER: 07/397,169
; FILING DATE: 08/21/89
; APPLICATION NUMBER: 07/376,555
; FILING DATE: 07/07/89
; APPLICATION NUMBER: 07/317,941
; FILING DATE: 03/02/89
; APPLICATION NUMBER: 07/282,328
; FILING DATE: 12/09/88
; APPLICATION NUMBER: 07/257,998
; FILING DATE: 10/14/88
; APPLICATION NUMBER: 07/248,771
; FILING DATE: 09/23/88
; APPLICATION NUMBER: 07/207,759
; FILING DATE: 06/16/88
; APPLICATION NUMBER: 07/204,171
; FILING DATE: 06/08/88
; APPLICATION NUMBER: 07/173,311
; FILING DATE: 03/25/88
; APPLICATION NUMBER: 07/100,571
; FILING DATE: 09/24/87
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00537/00900D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The sequence contains at
; OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,
; OTHER INFORMATION: and has an methyl ester C-terminus (i.e., COYCH3),
; OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., COYOH).
; US-08-337-127-8
;
; Query Match
; Best Local Similarity 84.0%; Score 21; DB 2; Length 8;
; Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 XQXXVXH 7
; Db 1 EQWAVGH 7
;
; RESULT 16
; US-09-260-846-4
; Sequence 4, Application US/09260846
; Patent No. 6307017
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun Hyuk
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
; FILE REFERENCE: 00537/00900J
; CURRENT APPLICATION NUMBER: US/09/260,846
; CURRENT FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
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; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: pyroglutamate
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: statine
; FEATURE:
; OTHER INFORMATION: this peptide has an amidated c-terminus
US-09-260-846-4

Query Match
Best Local Similarity 84.0%; Score 21; DB 4; Length 8;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXH 7
   ||::||
Db 1 EQWAVGH 7

RESULT 17
US-09-260-846-8
; Sequence 8, Application US/09260846
; Patent No. 6307017
; GENERAL INFORMATION:
; APPLICANT: COV, David H.
; APPLICANT: Moreau, Jacques-Pierre
; APPLICANT: Kim, Sun Hyuk
; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS
; FILE REFERENCE: 00537/00900J
; CURRENT APPLICATION NUMBER: US/09/260,846
; CURRENT FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: pyroglutamate
; FEATURE:
; OTHER INFORMATION: this peptide has a methyl ester c-terminus
US-09-260-846-8

Query Match
Best Local Similarity 84.0%; Score 21; DB 4; Length 8;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXH 7
   ||::||
Db 1 EQWAVGH 7

RESULT 18
US-09-248-381-6
; Sequence 6, Application US/09248381
; Patent No. 6492310
; GENERAL INFORMATION:
; APPLICANT: MURKOE, RAMA
; APPLICANT: JAGGI, MANU
; APPLICANT: PRASAD, SUDHANAND
; APPLICANT: BURMAN, ANAND C
; APPLICANT: RAJENDRAN, PRAVEEN
```

```
; APPLICANT: MATHUR, ARCHANA
; APPLICANT: SINGH, ANU T
; TITLE OF INVENTION: ANTITUMORIC DRUGS
; FILE REFERENCE: U:011695-8
; CURRENT APPLICATION NUMBER: US/09/248,381
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: This peptide
; OTHER INFORMATION: was synthetically generated.
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: /product=D-phenylalanine/label=D-Phe
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION:
US-09-248-381-6

Query Match
Best Local Similarity 84.0%; Score 21; DB 4; Length 8;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXH 7
   ||::||
Db 1 XQWAVGH 7

RESULT 19
5217955-31
; Patent No. 5217955
; APPLICANT: ABOGDE, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:31;
; LENGTH: 8
5217955-31

Query Match
Best Local Similarity 84.0%; Score 21; DB 6; Length 8;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXXXH 7
   ||::||
Db 1 XQWAVGH 7

RESULT 20
5217955-33
; Patent No. 5217955
; APPLICANT: ABOGDE, ARTHUR E.; MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
```

```

; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:33:
; LENGTH: 8
5217955-33

Query Match
Best Local Similarity 84.0%; Score 21; DB 6; Length 8;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXVXH 7
   :|:|:|
Db 1 EQWAVGH 7

RESULT 21
5217955-38
; Patent No. 5217955
; APPLICANT: ABOGDEH, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:38:
; LENGTH: 8
5217955-38

Query Match
Best Local Similarity 84.0%; Score 21; DB 6; Length 8;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXVXH 7
   :|:|:|
Db 1 EQWAVGH 7

RESULT 22
US-08-444-818-632
; Sequence 632, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 632:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-818-632

Query Match
Best Local Similarity 80.0%; Score 20; DB 3; Length 8;
Best Local Similarity 42.9%; Pred. No. 3e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXHI 8
   :|:|:|
Db 1 RKAVTTH 7

RESULT 23
5217955-37
; Patent No. 5217955
; APPLICANT: ABOGDEH, ARTHUR E.;MOREAU, JACQUES-PIERRE
; TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
; OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,225
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,039
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 408,125
; FILING DATE: 15-SEP-1989
; SEQ ID NO:37:
; LENGTH: 8
5217955-37

Query Match
Best Local Similarity 80.0%; Score 20; DB 6; Length 8;
Best Local Similarity 25.0%; Pred. No. 3e+05;
Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXVXHI 8
   :|:|:|
Db 1 FEWAVVHL 8

RESULT 24
US-08-444-818-633
; Sequence 633, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,818  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,590  
FILING DATE: 14-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hardin, Alisa A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 0110.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (508)359-3876  
TELEFAX: (508)359-3885  
INFORMATION FOR SEQ ID NO: 633:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-444-818-633

Query Match 76.0%; Score 19; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3e+05;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHI 8  
Db 1 KAVTHI 6

RESULT 25  
US-08-168-390-13  
Sequence 13, Application US/08168390  
Patent No. 5620955  
GENERAL INFORMATION:  
APPLICANT: Knight, Martha  
APPLICANT: Takahashi, Kazayuki  
TITLE OF INVENTION: Bombesin/Gastatin Releasing Peptide Antagonists  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/168,390  
FILING DATE: Herewith  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0871.0040001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
TELEX: 248636 SSK  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
FEATURE:

NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note= "The amino-terminal residue  
OTHER INFORMATION: comprises one of several chemical end caps."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: /note= "The carboxy-terminal  
OTHER INFORMATION: residue comprises an ethyl ester."  
US-08-168-390-13

Query Match 72.0%; Score 18; DB 1; Length 8;  
Best Local Similarity 25.0%; Pred. No. 3e+05;  
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXHI 8  
Db 1 NHWVGHL 8

RESULT 26  
US-08-168-390-14  
Sequence 14, Application US/08168390  
Patent No. 5620955  
GENERAL INFORMATION:  
APPLICANT: Knight, Martha  
APPLICANT: Takahashi, Kazayuki  
TITLE OF INVENTION: Bombesin/Gastatin Releasing Peptide Antagonists  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/168,390  
FILING DATE: Herewith  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0871.0040001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
TELEX: 248636 SSK  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note= "The amino-terminal residue  
OTHER INFORMATION: comprises one of several chemical end caps."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 6  
OTHER INFORMATION: /note= "The alanine at position 6  
OTHER INFORMATION: is dextrorotatory alanine."  
NAME/KEY: Modified-site  
LOCATION: 8  
OTHER INFORMATION: /note= "The carboxy-terminal

OTHER INFORMATION: residue comprises an ethyl ester."  
US-08-168-390-14  
Query Match  
Best Local Similarity 72.0%; Score 18; DB 1; Length 8;  
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 1 XQXXVXHI 8  
DB 1 NHWVAHL 8  
RESULT 27  
US-08-178-268-16  
Sequence 16, Application US/08178268  
Patent No. 5795859  
GENERAL INFORMATION:  
APPLICANT: RATHGEN, Deborah A  
APPLICANT: WIDMER, Fred  
APPLICANT: GRIGG, Geoffrey W  
APPLICANT: MACK, Philip O  
TITLE OF INVENTION: Peptide which Abrogates TNF and/or LPS Toxicity  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye P.C.  
STREET: 1100 No. 5795859th Giebe Road, 8th Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/178,268  
FILING DATE: 05-JAN-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: MITCHARD, Leonard C  
REGISTRATION NUMBER: 29,009  
REFERENCE/DOCKET NUMBER: 47-45  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: both  
MOLECULE TYPE: peptide  
US-08-178-268-16  
Query Match  
Best Local Similarity 72.0%; Score 18; DB 1; Length 8;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 3 XXVXHI 8  
DB 1 KPVAVH 6  
RESULT 28  
US-09-082-279B-1459  
Sequence 1459, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1459  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HIV-1  
US-09-082-279B-1459  
Query Match  
Best Local Similarity 72.0%; Score 18; DB 3; Length 8;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 1 XQXXVXHI 8  
DB 1 WQWMDQHI 8  
RESULT 29  
US-09-315-304B-1612  
Sequence 1612, Application US/09315304B  
Patent No. 6348568  
GENERAL INFORMATION:  
APPLICANT: Barney, S.  
APPLICANT: Merutka, G.  
APPLICANT: Anwer, M.  
APPLICANT: Lambert, D.  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
FILE REFERENCE: 7872-052  
CURRENT APPLICATION NUMBER: US/09/315,304B  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1612  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HIV-1  
US-09-315-304B-1612  
Query Match  
Best Local Similarity 72.0%; Score 18; DB 4; Length 8;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 1 XQXXVXHI 8  
DB 1 WQWMDQHI 8  
RESULT 30  
US-09-834-784-1459  
Sequence 1459, Application US/09834784  
Patent No. 6362787  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/834,784  
CURRENT FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 1459  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HIV-1  
US-09-834-784-1459

Query Match 72.0%; Score 18; DB 4; Length 8;  
Best Local Similarity 37.5%; Pred. No. 3e+05;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXHI 8  
:|:|:|  
1 WQWMDQHI 8

RESULT 31  
US-09-350-641C-1613  
Sequence 1613 Application US/09350641C  
Patent No. 6656906  
GENERAL INFORMATION:  
APPLICANT: Barney, S.  
APPLICANT: Guthrie, K.  
APPLICANT: Merutka, G.  
APPLICANT: Anwer, M.  
APPLICANT: Lambert, D.  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
FILE REFERENCE: 7872-067  
CURRENT APPLICATION NUMBER: US/09/350,641C  
CURRENT FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: 09/315,304  
PRIOR FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1757  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 1613  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HIV-1  
US-09-350-641C-1613

Query Match 72.0%; Score 18; DB 4; Length 8;  
Best Local Similarity 37.5%; Pred. No. 3e+05;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXHI 8  
:|:|:|  
1 WQWMDQHI 8

RESULT 32  
US-08-387-634-3  
Sequence 3 Application US/08387634  
Patent No. 5767236  
GENERAL INFORMATION:  
APPLICANT: Kim, Sun Hyuk  
APPLICANT: Moreau, Jacques-Pierre  
TITLE OF INVENTION: LINEAR THERAPEUTIC PEPTIDES  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/387,634  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/929,306A  
FILING DATE: 08/13/92  
APPLICATION NUMBER: US/07/520,226  
FILING DATE: 05/09/90  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T. and Tsao, Y. Rocky  
REGISTRATION NUMBER: 30,162 and 34,053  
REFERENCE/DOCKET NUMBER: 00537/040002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8  
TYPE: amino acid  
STRANDEDNESS: N/A  
TOPOLOGY: N/A  
FEATURE:  
OTHER INFORMATION:  
OTHER INFORMATION: The sequence contains at position 1 an acetylated His, rather  
than a His, and has an amide C-terminus (i.e., COOH).  
US-08-387-634-3

Query Match 68.0%; Score 17; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 3e+05;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXHI 8  
:|:|:|  
2 WAVGHL 7

RESULT 33  
US-08-816-346-20  
Sequence 20 Application US/08816346  
Patent No. 6127525  
GENERAL INFORMATION:  
APPLICANT: Crystal, Ronald G.  
APPLICANT: Falck-Pedersen, Erik  
APPLICANT: Gall, Jason  
APPLICANT: Kovsedl, Imre  
APPLICANT: Wickham, Thomas J.  
TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND  
METHODS OF USING SAME  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.  
STREET: TWO PRUDENTIAL PLAZA - 4900  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: USA  
ZIP: 60601-6780  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #110, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,346  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
REFERENCE/DOCKET NUMBER: 67167  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/616-5600

TELEFAX: 312/616-5700  
TELEX: 25-3533  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-816-346-20

Query Match 68.0%; Score 17; DB 3; Length 8;  
Best Local Similarity 14.3%; Pred. No. 3e+05;  
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXVXH 7  
Db 1 YETEHNH 7

RESULT 34  
US-09-335-411-20

Sequence 20, Application US/09335411  
Patent No. 6153435

GENERAL INFORMATION:

APPLICANT: Crystal, Ronald G.  
APPLICANT: Falck-Pedersen, Erik

APPLICANT: Gall, Jason

APPLICANT: Kovesam, Imre

APPLICANT: Micham, Thomas J.

TITLE OF INVENTION: CHIMERIC ADENOVIRAL COAT PROTEIN AND  
METHODS OF USING SAME

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:  
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.

STREET: TWO PRUDENTIAL PLAZA - 4900  
CITY: CHICAGO

STATE: ILLINOIS

COUNTRY: USA

ZIP: 60601-6780

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/335,411

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/816,346

FILING DATE:

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 67167

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/616-5600

TELEFAX: 312/616-5700

TELEX: 25-3533

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-335-411-20

Query Match 68.0%; Score 17; DB 3; Length 8;  
Best Local Similarity 14.3%; Pred. No. 3e+05;  
Matches 1; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXXVXH 7  
Db 1 YETEHNH 7

RESULT 35  
US-09-515-965A-1846  
Sequence 1846, Application US/09515965A  
Patent No. 6623741

GENERAL INFORMATION:

APPLICANT: Antczak, J.

APPLICANT: Delmedico, M.

APPLICANT: Erickson, J.

APPLICANT: Lambert, D.

APPLICANT: Sista, P.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-  
ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION

FILE REFERENCE: 7872-073

CURRENT FILING DATE: 2000-02-29

PRIOR APPLICATION NUMBER: 09/315,304

PRIOR FILING DATE: 1998-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1994

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1846

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-515-965A-1846

Query Match 68.0%; Score 17; DB 4; Length 8;  
Best Local Similarity 33.3%; Pred. No. 3e+05;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 8  
Db 3 SKVLHL 8

RESULT 36  
5217955-25

Patent No. 5217955

APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE

TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG

OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN

NUMBER OF SEQUENCES: 42

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/520,225

FILING DATE: 09-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 440,039

FILING DATE: 21-NOV-1989

APPLICATION NUMBER: 408,125

FILING DATE: 15-SEP-1989

SEQ ID NO: 25

LENGTH: 8

5217955-25

Query Match 68.0%; Score 17; DB 6; Length 8;  
Best Local Similarity 33.3%; Pred. No. 3e+05;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 8  
Db 2 WAAVHL 7

RESULT 37  
5217955-27

Patent No. 5217955

APPLICANT: ABOGDEN, ARTHUR E.; MOREAU, JACQUES-PIERRE

TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG

OF BOMBESIN, GRP, LITORIN OR NEUROMEDIN



NUMBER OF SEQUENCES: 42  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,225  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 440,039  
FILING DATE: 21-NOV-1989  
APPLICATION NUMBER: 408,125  
FILING DATE: 15-SEP-1989  
SEQ ID NO:27:  
LENGTH: 8  
5217955-27

Query Match 68.0%; Score 17; DB 6; Length 8;  
Best Local Similarity 33.3%; Pred. No. 3e+05;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH1 8  
: : : :  
Db 2 WAGVHL 7

RESULT 38  
5217955-28  
Patent No. 5217955  
APPLICANT: ABOGDEH, ARTHUR E.; MOREAU, JACQUES-PIERRE  
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG  
OF BOMBESIN, GRP, LITORIN OR NEURMEDIN  
NUMBER OF SEQUENCES: 42  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,225  
FILING DATE: 09-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 440,039  
FILING DATE: 21-NOV-1989  
APPLICATION NUMBER: 408,125  
FILING DATE: 15-SEP-1989  
SEQ ID NO:28:  
LENGTH: 8  
5217955-28

Query Match 68.0%; Score 17; DB 6; Length 8;  
Best Local Similarity 33.3%; Pred. No. 3e+05;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH1 8  
: : : :  
Db 2 WAGVHL 7

RESULT 39  
US-08-457-804-5  
Sequence 5, Application US/08457804  
Patent No. 5618785  
GENERAL INFORMATION:  
APPLICANT: Heavener, George A.  
APPLICANT: Kruszynski, Marian  
APPLICANT: Mervic, Miljenko  
TITLE OF INVENTION: Peptide Inhibitors of Selectin  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
ADDRESSEE: and No. 5618785tlb  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,804  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/156,415  
FILING DATE: No. 5618785ember 22, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Dianne B. Elderkin  
REGISTRATION NUMBER: 28,598  
REFERENCE/DOCKET NUMBER: CCOR-0136  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acid residues  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-457-804-5

Query Match 64.0%; Score 16; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 3e+05;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH1 8  
: : : :  
Db 2 TKLVH1 7

RESULT 40  
US-08-843-035-16  
Sequence 16, Application US/08843035  
Patent No. 5783662  
GENERAL INFORMATION:  
APPLICANT: Janney, Paul A.  
APPLICANT: Cunningham, C. Casey  
APPLICANT: Hartwig, John H.  
APPLICANT: Stossel, Thomas P.  
APPLICANT: Vegner, Roland  
TITLE OF INVENTION: POLYPHOSPHONOSITIDE BINDING  
TITLE OF INVENTION: PEPTIDES FOR INTRACELLULAR DRUG DELIVERY  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: Federal Reserve Plaza, 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/843,035  
FILING DATE: 11-APR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/394,027  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Plumer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: B0801/7029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-843-035-16

Query Match 64.0%; Score 16; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. No. 3e+05;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7  
:::|:  
DB 1 KILVXH 6

RESULT 41  
US-08-178-268-10  
Sequence 10, Application US/08178268  
Patent No. 5795859  
GENERAL INFORMATION:  
APPLICANT: RATHGEM, Deborah A  
APPLICANT: WIDMER, Fred  
APPLICANT: GRIGG, Geoffrey W  
APPLICANT: MACK, Philip O  
TITLE OF INVENTION: Peptide which Abrogates TNF and/or LPS Toxicity  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Nixon & Vanderhye P.C.  
STREET: 1100 No. 5795859th Glebe Road, 8th Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/178,268  
FILING DATE: 05-JAN-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: MITCHARD, Leonard C  
REGISTRATION NUMBER: 29,009  
REFERENCE/DOCKET NUMBER: 47-45  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: both  
MOLECULE TYPE: peptide  
US-08-178-268-10

Query Match 64.0%; Score 16; DB 1; Length 8;  
Best Local Similarity 28.6%; Pred. No. 3e+05;  
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXH 7  
:::|:  
DB 2 SDKPVXH 8

RESULT 42  
US-07-885-089B-25  
Sequence 25, Application US/07885089B  
Patent No. 5830995

GENERAL INFORMATION:  
APPLICANT: Shoyab, Mohammed  
APPLICANT: McDonald, Vicki L.  
APPLICANT: Bradley, James G.  
APPLICANT: Plowman, Gregory D.  
TITLE OF INVENTION: AMPHIREGULINS. A FAMILY OF  
TITLE OF INVENTION: HEPARIN-BINDING EPITHELIAL CELL GROWTH FACTORS  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Penite & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/885,089B  
FILING DATE: 18-MAY-1992  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 5624-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-885-089B-25

Query Match 64.0%; Score 16; DB 2; Length 8;  
Best Local Similarity 28.6%; Pred. No. 3e+05;  
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXH 7  
:::|:  
DB 1 FQNFCTH 7

RESULT 43  
US-08-755-496A-16  
Sequence 16, Application US/08755496A  
Patent No. 5846743

GENERAL INFORMATION:  
APPLICANT: Cunningham, Casey  
APPLICANT: Hartwig, John H.  
APPLICANT: Janney, Paul A.  
APPLICANT: Scossel, Thomas P.  
TITLE OF INVENTION: POLYPHOSPHOINOSTITIDE-(PPI-) BINDING  
TITLE OF INVENTION: PEPTIDE(S) FOR INTRACELLULAR DRUG DELIVERY  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wolf, Greenfield & Sacke, P.C.  
STREET: Federal Reserve Plaza, 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,496A
; FILING DATE: 22-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/394,027
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-755-496A-16

Query Match      64.0%; Score 16; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      2 QXXVXH 7
      ::::|
Db      1 KILVKH 6

RESULT 44
US-08-925-002-37
; Sequence 37, Application US/08925002
; Patent No. 6048527
; GENERAL INFORMATION:
; APPLICANT: Granoff, Dan M.
; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
; FILE REFERENCE: 1238.002
; CURRENT APPLICATION NUMBER: US/08/925.002
; CURRENT FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence from
; US-08-925-002-37

Query Match      64.0%; Score 16; DB 3; Length 8;
Best Local Similarity 28.6%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 XQXXVXH 7
      ::::|
Db      1 LNFKVRH 7

RESULT 45
US-08-444-818-432
; Sequence 432, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
```

```

; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hardin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 432:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-444-818-432

Query Match      64.0%; Score 16; DB 3; Length 8;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 XXVXHI 8
      ::::|
Db      3 IGLIHI 8

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Job time : 13.5 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2004, 15:51:28 ; Search time 38 Seconds  
(without alignments)  
66.159 Million cell updates/sec

Title: VARIANT2  
Perfect score: 25  
Sequence: 1 XQXXVXHI 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 16665

Minimum DB seq length: 8  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:\*  
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2: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppa/US05\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppa/US04\_PUBCOMB.pep:\*  
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11: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/1/pubppa/US03\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	92.0	8	10	US-09-896-903C-2
2	23	92.0	8	14	US-10-182-252A-948
3	23	92.0	8	16	US-10-182-252A-950
4	22	88.0	8	9	US-09-896-903C-2
5	22	88.0	8	10	US-09-896-903C-2
6	22	88.0	8	14	US-10-182-252A-948
7	22	88.0	8	16	US-10-182-252A-950
8	21	84.0	8	14	US-10-182-252A-948
9	19	76.0	8	12	US-10-182-252A-946
10	19	76.0	8	12	US-10-182-252A-946
11	19	76.0	8	12	US-10-182-252A-946
12	19	76.0	8	12	US-10-182-252A-946
13	19	76.0	8	12	US-10-182-252A-946
14	19	76.0	8	12	US-10-182-252A-946
15	19	76.0	8	12	US-10-182-252A-946

16	19	76.0	8	12	US-10-182-252A-947	Sequence 947, App
17	19	76.0	8	12	US-10-182-252A-948	Sequence 948, App
18	19	76.0	8	12	US-10-182-252A-950	Sequence 950, App
19	19	76.0	8	12	US-10-182-252A-951	Sequence 951, App
20	19	76.0	8	12	US-10-182-252A-1285	Sequence 1285, App
21	18	72.0	8	12	US-10-187-957-6	Sequence 6, App11
22	18	72.0	8	14	US-10-351-641-1613	Sequence 1613, App
23	18	72.0	8	16	US-10-387-934-6	Sequence 6, App1
24	17	68.0	8	10	US-09-876-904A-181	Sequence 181, App1
25	17	68.0	8	12	US-10-387-957-7	Sequence 7, App11
26	17	68.0	8	12	US-10-014-340-64	Sequence 64, App1
27	17	68.0	8	12	US-10-182-252A-624	Sequence 624, App
28	17	68.0	8	12	US-10-182-252A-625	Sequence 625, App
29	17	68.0	8	12	US-10-328-953-94	Sequence 94, App1
30	17	68.0	8	12	US-10-367-580-186	Sequence 186, App
31	17	68.0	8	12	US-10-367-580-234	Sequence 234, App
32	17	68.0	8	12	US-10-367-593-186	Sequence 186, App
33	17	68.0	8	12	US-10-367-593-234	Sequence 234, App
34	17	68.0	8	12	US-10-367-594-186	Sequence 186, App
35	17	68.0	8	12	US-10-367-594-234	Sequence 234, App
36	17	68.0	8	12	US-10-367-654-186	Sequence 186, App
37	17	68.0	8	12	US-10-367-654-234	Sequence 234, App
38	17	68.0	8	12	US-10-367-658-186	Sequence 186, App
39	17	68.0	8	12	US-10-367-658-234	Sequence 234, App
40	17	68.0	8	12	US-10-367-668-186	Sequence 186, App
41	17	68.0	8	12	US-10-367-668-234	Sequence 234, App
42	17	68.0	8	14	US-10-139-146-66	Sequence 66, App1
43	17	68.0	8	14	US-10-052-578-13	Sequence 13, App1
44	17	68.0	8	14	US-10-053-520-13	Sequence 13, App1
45	17	68.0	8	14	US-10-053-498B-13	Sequence 13, App1

#### ALIGNMENTS

RESULT 1  
US-09-896-903C-2  
Sequence 2, App11  
Publication No. US20030050233A1  
GENERAL INFORMATION:  
APPLICANT: Burman, Anand C.  
APPLICANT: Mukherjee, Rama  
APPLICANT: Prasad, Suchanand  
APPLICANT: Jaggi, Manu  
TITLE OF INVENTION: PEPTIDE COMBINATION FOR TREATMENT OF CANCER  
FILE REFERENCE: 0132970  
CURRENT APPLICATION NUMBER: US/09/896,903C  
CURRENT FILING DATE: 2001-06-29  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: This peptide  
OTHER INFORMATION: was synthetically generated.  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (1)  
OTHER INFORMATION: /product = Butanoyl D-phenylalanine/label =  
OTHER INFORMATION: Butanoyl-D-Phe  
NAME/KEY: MOD RES  
LOCATION: (6)  
OTHER INFORMATION: / product = alpha-Aminoisobutyric acid/label = Alb  
US-09-896-903C-2  
Query Match 92.0%; Score 23; DB 10; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1.2e+06;  
Matches 5; Conservative 3; Mismatches 0; Gaps 0;

Qy 1 XQXXVXHI 8  
Db 1 XQWAVXHL 8

## RESULT 2

US-10-186-226A-2  
Sequence 2, Application US/10186226A  
Publication No. US20030105009A1  
GENERAL INFORMATION:  
APPLICANT: Prasad, Sudhanand  
APPLICANT: Mukherjee, Rama  
APPLICANT: Burman, Anand C.  
APPLICANT: Mathur, Archana  
APPLICANT: Sharma, Rajan  
APPLICANT: Jaggi, Manu  
TITLE OF INVENTION: POLYPEPTIDES OF COVALENTLY LINKED SYNTHETIC BIOACTIVE PEPTIDE ANALOGS FOR THE TREATMENT OF CANCER  
FILE REFERENCE: U 014073-7  
CURRENT APPLICATION NUMBER: US/10/186,226A  
CURRENT FILING DATE: 2002-08-16  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: This peptide was synthetically generated  
NAME/KEY: MISC FEATURE  
LOCATION: (1)..(1)  
OTHER INFORMATION: /product = D-Phenylalanine/label = D-Phe  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (6)..(6)  
OTHER INFORMATION: /product = Alpha-amino-isobutyric acid/label = Alb  
US-10-186-226A-2

## Query Match

Best Local Similarity 92.0%; Score 23; DB 14; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1.2e+06;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XQXXVXHI 8  
Db 1 XQWAVXHL 8

## RESULT 3

US-10-329-321A-2  
Sequence 2, Application US/10329321A  
Publication No. US20040121950A1  
GENERAL INFORMATION:  
APPLICANT: Mukherjee, Rama  
APPLICANT: Burman, Anand  
APPLICANT: Singh, Anu  
APPLICANT: Jaggi, Manu  
APPLICANT: Prasad, Sudhanand  
APPLICANT: Dutt, Sarjana  
TITLE OF INVENTION: A DRUG COMPRISING SYNTHETIC PEPTIDE ANALOGS FOR THE TREATMENT OF CANCER  
FILE REFERENCE: U 014319-1  
CURRENT APPLICATION NUMBER: US/10/329,321A  
CURRENT FILING DATE: 2002-12-23  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: This peptide was synthetically generated  
FEATURE:

NAME/KEY: MISC FEATURE  
LOCATION: (1)..(1)  
OTHER INFORMATION: /product = D-phenylalanine/label = D-Phe  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (6)..(6)  
OTHER INFORMATION: /product = 2-amino-isobutyric acid/label = Alb  
US-10-329-321A-2

Query Match  
Best Local Similarity 92.0%; Score 23; DB 16; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1.2e+06;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 XQXXVXHI 8  
Db 1 XQWAVXHL 8

## RESULT 4

US-09-766-347-1  
Sequence 1, Application US/09766347  
Patent No. US20020169107A1  
GENERAL INFORMATION:  
APPLICANT: Rajagopalan, Raghavan  
APPLICANT: Cantrell, Gary  
APPLICANT: Achilefu, Samuel  
APPLICANT: Bugaj, Joseph  
APPLICANT: Dorschow, Richard  
TITLE OF INVENTION: NOVEL AROMATIC AZIDES FOR TYPE I PHOTOTHERAPY  
FILE REFERENCE: MRD-60  
CURRENT APPLICATION NUMBER: US/09/766,347  
CURRENT FILING DATE: 2001-01-19  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: Patent In Version 3.1  
SEQ ID NO 1  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (1)..(8)  
OTHER INFORMATION: Bombesin analog  
US-09-766-347-1

Query Match  
Best Local Similarity 88.0%; Score 22; DB 9; Length 8;  
Best Local Similarity 42.9%; Pred. No. 1.2e+06;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QXXVXHI 8  
Db 1 QWAVGHL 7

## RESULT 5

US-09-898-887B-1  
Sequence 1, Application US/09898887B  
Publication No. US20030158127A1  
GENERAL INFORMATION:  
APPLICANT: Mallinckrodt Inc.  
APPLICANT: Rajagopalan, Raghavan  
APPLICANT: Cantrell, Gary  
APPLICANT: Achilefu, Samuel I.  
APPLICANT: Bugaj, Joseph  
APPLICANT: Dorschow, Richard  
TITLE OF INVENTION: AROMATIC SULFONATES FOR TYPE I PHOTOTHERAPY  
FILE REFERENCE: MRD-61  
CURRENT APPLICATION NUMBER: US/09/898,887B  
CURRENT FILING DATE: 2001-07-03  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1  
LENGTH: 8

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: The sulfente-bombesin (7-14) conjugate has the following  
OTHER INFORMATION: molecular structure:  
OTHER INFORMATION: p-azidocetatefluorobenzoyl-Gln-Trp-Ala-Val-Gly-His-Leu-Met-NH<sub>2</sub>.  
US-09-898-887B-1

Query Match 88.0%; Score 22; DB 10; Length 8;  
Best Local Similarity 42.9%; Pred. No. 1.2e+06; Indels 0; Gaps 0;  
Matches 3; Conservative 4; Mismatches 0;

QY 2 QXXVXH1 8  
DB 1 QMAVGH1 7

RESULT 6  
US-10-281-840-2  
Sequence 2, Application US/10281840  
Publication No. US20030082192A1  
GENERAL INFORMATION:  
APPLICANT: Safavy, Ahmad  
TITLE OF INVENTION: Multidrug Multiligand Conjugates for Targeted Drug Delivery  
FILE REFERENCE: P66788US01GP  
CURRENT APPLICATION NUMBER: US/10/281,840  
CURRENT FILING DATE: 2002-10-28  
PRIOR APPLICATION NUMBER: US 60/348,299  
PRIOR FILING DATE: 2001-10-26  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-281-840-2

Query Match 88.0%; Score 22; DB 14; Length 8;  
Best Local Similarity 42.9%; Pred. No. 1.2e+06; Indels 0; Gaps 0;  
Matches 3; Conservative 4; Mismatches 0;

QY 2 QXXVXH1 8  
DB 1 QMAVGH1 7

RESULT 7  
US-10-341-577-1  
Sequence 1, Application US/10341577  
Publication No. US20040136906A1  
GENERAL INFORMATION:  
APPLICANT: Bracco Research U.S.A.  
TITLE OF INVENTION: Improved Gastrin Releasing Peptide Compounds  
FILE REFERENCE: 57637-1020  
CURRENT APPLICATION NUMBER: US/10/341,577  
CURRENT FILING DATE: 2003-01-13  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 1  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: This peptide is the receptor  
OTHER INFORMATION: binding site of bombesin and is also known as BBN[7-14]  
US-10-341-577-1

Query Match 88.0%; Score 22; DB 16; Length 8;  
Best Local Similarity 42.9%; Pred. No. 1.2e+06; Indels 0; Gaps 0;  
Matches 3; Conservative 4; Mismatches 0;

QY 2 QXXVXH1 8

DB 1 QMAVGH1 7

RESULT 8  
US-10-004-530A-4  
Sequence 4, Application US/10004530A  
Publication No. US20030050436A1  
GENERAL INFORMATION:  
APPLICANT: Coy, David H.  
APPLICANT: Moreau, Jacques-Pierre  
APPLICANT: Kim, Sun H.  
TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN ANALOGS  
FILE REFERENCE: 00537-00900K  
CURRENT APPLICATION NUMBER: US/10/004,530A  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 09/260,846  
PRIOR FILING DATE: 1999-03-02  
PRIOR APPLICATION NUMBER: 08/337,127  
PRIOR FILING DATE: 1994-11-10  
PRIOR APPLICATION NUMBER: 07/779,039  
PRIOR FILING DATE: 1991-10-18  
PRIOR APPLICATION NUMBER: 07/502,438  
PRIOR FILING DATE: 1990-03-30  
PRIOR APPLICATION NUMBER: 07/397,169  
PRIOR FILING DATE: 1989-08-21  
PRIOR APPLICATION NUMBER: 07/376,555  
PRIOR FILING DATE: 1989-07-07  
PRIOR APPLICATION NUMBER: 07/317,941  
PRIOR FILING DATE: 1989-03-02  
PRIOR APPLICATION NUMBER: 07/282,328  
PRIOR FILING DATE: 1988-12-09  
PRIOR APPLICATION NUMBER: 07/257,998  
PRIOR FILING DATE: 1988-10-14  
PRIOR APPLICATION NUMBER: 07/248,771  
PRIOR FILING DATE: 1988-09-23  
Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
NAME/KEY: VARIANT  
LOCATION: 8  
OTHER INFORMATION: Xaa = statine  
US-10-004-530A-4

Query Match 84.0%; Score 21; DB 14; Length 8;  
Best Local Similarity 42.9%; Pred. No. 1.2e+06; Indels 0; Gaps 0;  
Matches 3; Conservative 4; Mismatches 0;

QY 1 XOXVXH 7  
DB 1 EQMAVGH 7

RESULT 9  
US-10-182-252A-322  
Sequence 322, Application US/10182252A  
Publication No. US20040072162A1  
GENERAL INFORMATION:  
APPLICANT: FOMSGARD, ANDERS  
APPLICANT: BRUNAK, SOREN  
APPLICANT: BUIS, SOREN  
APPLICANT: CORBET, SYLVIE  
APPLICANT: LAUBMOLLER, SANNE LISE  
APPLICANT: HANSEN, JAN  
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
FILE REFERENCE: 030307/0205

```
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 322
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-322

Query Match
Best Local Similarity 33.3%; Score 19; DB 12; Length 8;
Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 2 OXXVXH 7
Db 1 QIGIPH 6

RESULT 10
US-10-182-252A-940
; Sequence 940, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 940
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-940

Query Match
Best Local Similarity 33.3%; Score 19; DB 12; Length 8;
Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 2 OXXVXH 7
Db 1 QIGIPH 6

RESULT 11
US-10-182-252A-941
; Sequence 941, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
```

```
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 941
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-941

Query Match
Best Local Similarity 33.3%; Score 19; DB 12; Length 8;
Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 2 OXXVXH 7
Db 1 QIGIPH 6

RESULT 12
US-10-182-252A-942
; Sequence 942, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 942
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-942

Query Match
Best Local Similarity 33.3%; Score 19; DB 12; Length 8;
Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 2 OXXVXH 7
```



Db 1 QIGIPH 6

RESULT 13

US-10-182-252A-943

Sequence 943, Application US/10182252A

Publication No. US20040072162A1

GENERAL INFORMATION:

APPLICANT: FOMSGAARD, ANDERS

APPLICANT: BRUNAK, SOREN

APPLICANT: BUUS, SOREN

APPLICANT: CORBET, SYLVIE

APPLICANT: LAUEMOLLER, SANNE LISE

APPLICANT: HANSEN, JAN

TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND

CONTROL OF HIV INFECTIONS

FILE REFERENCE: 030307/0205

CURRENT APPLICATION NUMBER: US/10/182,252A

PRIOR FILING DATE: 2003-04-10

PRIOR APPLICATION NUMBER: PCT/DK01/00059

PRIOR FILING DATE: 2001-01-29

PRIOR APPLICATION NUMBER: EP 00610017.6

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: US 60/179,333

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 1388

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 943

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: HIV peptide

US-10-182-252A-943

Query Match 76.0%; Score 19; DB 12; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7

Db 1 QIGIPH 6

RESULT 14

US-10-182-252A-944

Sequence 944, Application US/10182252A

Publication No. US20040072162A1

GENERAL INFORMATION:

APPLICANT: FOMSGAARD, ANDERS

APPLICANT: BRUNAK, SOREN

APPLICANT: BUUS, SOREN

APPLICANT: CORBET, SYLVIE

APPLICANT: LAUEMOLLER, SANNE LISE

APPLICANT: HANSEN, JAN

TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND

CONTROL OF HIV INFECTIONS

FILE REFERENCE: 030307/0205

CURRENT APPLICATION NUMBER: US/10/182,252A

PRIOR FILING DATE: 2003-04-10

PRIOR APPLICATION NUMBER: PCT/DK01/00059

PRIOR FILING DATE: 2001-01-29

PRIOR APPLICATION NUMBER: EP 00610017.6

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: US 60/179,333

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 1388

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 944

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide

US-10-182-252A-944

Query Match 76.0%; Score 19; DB 12; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7

Db 1 QIGIPH 6

RESULT 15

US-10-182-252A-946

Sequence 946, Application US/10182252A

Publication No. US20040072162A1

GENERAL INFORMATION:

APPLICANT: FOMSGAARD, ANDERS

APPLICANT: BRUNAK, SOREN

APPLICANT: BUUS, SOREN

APPLICANT: CORBET, SYLVIE

APPLICANT: LAUEMOLLER, SANNE LISE

APPLICANT: HANSEN, JAN

TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND

CONTROL OF HIV INFECTIONS

FILE REFERENCE: 030307/0205

CURRENT APPLICATION NUMBER: US/10/182,252A

PRIOR FILING DATE: 2003-04-10

PRIOR APPLICATION NUMBER: PCT/DK01/00059

PRIOR FILING DATE: 2001-01-29

PRIOR APPLICATION NUMBER: EP 00610017.6

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: US 60/179,333

PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 1388

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 946

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: HIV peptide

US-10-182-252A-946

Query Match 76.0%; Score 19; DB 12; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7

Db 1 QIGIPH 6

RESULT 16

US-10-182-252A-947

Sequence 947, Application US/10182252A

Publication No. US20040072162A1

GENERAL INFORMATION:

APPLICANT: FOMSGAARD, ANDERS

APPLICANT: BRUNAK, SOREN

APPLICANT: BUUS, SOREN

APPLICANT: CORBET, SYLVIE

APPLICANT: LAUEMOLLER, SANNE LISE

APPLICANT: HANSEN, JAN

TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND

CONTROL OF HIV INFECTIONS

FILE REFERENCE: 030307/0205

CURRENT APPLICATION NUMBER: US/10/182,252A

PRIOR FILING DATE: 2003-04-10

PRIOR APPLICATION NUMBER: PCT/DK01/00059

PRIOR FILING DATE: 2001-01-29

PRIOR APPLICATION NUMBER: EP 00610017.6

```

; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 947
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-947
```

```

Query Match      76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
       |:::|
Db      1 QMGIPH 6
```

```

RESULT 17
US-10-182-252A-948
; Sequence 948, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUTS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 948
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-948
```

```

Query Match      76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
       |:::|
Db      1 QMGIPH 6
```

```

RESULT 18
US-10-182-252A-950
; Sequence 950, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUTS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: LAUEMOLLER, SANNE LISE
```

```

; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 950
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-950
```

```

Query Match      76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
       |:::|
Db      1 QMGIPH 6
```

```

RESULT 19
US-10-182-252A-951
; Sequence 951, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUTS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 951
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-951
```

```

Query Match      76.0%; Score 19; DB 12; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 QXXVXH 7
       |:::|
Db      1 QMGIPH 6
```

```
RESULT 20
```

US-10-182-252A-1285  
 ; Sequence 1285, Application US/10182252A  
 ; Publication No. US20040072162A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FOMSGAARD, ANDERS  
 ; APPLICANT: BRUNAK, SOREN  
 ; APPLICANT: BUS, SOREN  
 ; APPLICANT: CORBET, SYLVIE  
 ; APPLICANT: LAUEWOLLER, SANNE LISE  
 ; APPLICANT: HANSEN, JAN  
 ; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
 ; FILE OF INVENTION: CONTROL OF HIV INFECTIONS  
 ; FILE REFERENCE: 030307/0205  
 ; CURRENT APPLICATION NUMBER: US/10/182,252A  
 ; PRIOR FILING DATE: 2003-04-10  
 ; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
 ; PRIOR FILING DATE: 2001-01-29  
 ; PRIOR APPLICATION NUMBER: EP 00610017.6  
 ; PRIOR FILING DATE: 2000-01-28  
 ; PRIOR APPLICATION NUMBER: US 60/179,333  
 ; PRIOR FILING DATE: 2000-01-31  
 ; NUMBER OF SEQ ID NOS: 138  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1285  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus  
 US-10-182-252A-1285

Query Match 76.0%; Score 19; DB 12; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7  
 Db 1 QLGIPH 6

RESULT 21  
 US-10-387-957-6  
 ; Sequence 6, Application US/10387957  
 ; Publication No. US20040052809A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GlaxoSmithKline Biologicals s.a.  
 ; TITLE OF INVENTION: Vaccine  
 ; FILE REFERENCE: B45284  
 ; CURRENT APPLICATION NUMBER: US/10/387,957  
 ; CURRENT FILING DATE: 2003-03-13  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 6  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-387-957-6

Query Match 72.0%; Score 18; DB 12; Length 8;  
 Best Local Similarity 28.6%; Pred. No. 1.2e+06;  
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7  
 Db 1 MCGYMKH 7

RESULT 22  
 US-10-351-641-1613  
 ; Sequence 1613, Application US/10351641  
 ; Publication No. US20030186874A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Barney, S.  
 ; APPLICANT: Guthrie, K.  
 ; APPLICANT: Merutka, G.

APPLICANT: Anwer, M.  
 ; APPLICANT: Lambert, D.  
 ; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
 ; TITLE OF INVENTION: PROPERTIES  
 ; FILE REFERENCE: 7872-100  
 ; CURRENT APPLICATION NUMBER: US/10/351,641  
 ; CURRENT FILING DATE: 2003-01-24  
 ; PRIOR APPLICATION NUMBER: 09/350,641  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: 09/315,304  
 ; PRIOR FILING DATE: 1999-05-20  
 ; PRIOR APPLICATION NUMBER: 09/082,279  
 ; PRIOR FILING DATE: 1998-05-20  
 ; NUMBER OF SEQ ID NOS: 1757  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1613  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: HIV-1  
 US-10-351-641-1613

Query Match 72.0%; Score 18; DB 14; Length 8;  
 Best Local Similarity 37.5%; Pred. No. 1.2e+06;  
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XQXXVXH 8  
 Db 1 WOQMDQHI 8

RESULT 23  
 US-10-387-934-6  
 ; Sequence 6, Application US/10387934  
 ; Publication No. US20040091496A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mettens, Pascal  
 ; APPLICANT: Meykens, Rene  
 ; APPLICANT: Montevne, Philippe  
 ; TITLE OF INVENTION: Vaccine  
 ; FILE REFERENCE: VB60137  
 ; CURRENT APPLICATION NUMBER: US/10/387,934  
 ; CURRENT FILING DATE: 2003-03-13  
 ; PRIOR APPLICATION NUMBER: PCT/EP02/09650  
 ; PRIOR FILING DATE: 2002-08-29  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 6  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-387-934-6

Query Match 72.0%; Score 18; DB 16; Length 8;  
 Best Local Similarity 28.6%; Pred. No. 1.2e+06;  
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7  
 Db 1 MCGYMKH 7

RESULT 24  
 US-09-876-904A-181  
 ; Sequence 181, Application US/09876904A  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TEVI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIGASES TM) AND THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
 ; FILE REFERENCE: TB-2002.00  
 ; CURRENT APPLICATION NUMBER: US/09/876,904A  
 ; CURRENT FILING DATE: 2001-06-08

;; PRIOR APPLICATION NUMBER: US 60/210,925  
;; PRIOR FILING DATE: 2000-06-09  
;; NUMBER OF SEQ ID NOS: 629  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 181  
;; LENGTH: 8  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: Karyophilic peptide  
US-09-876-904A-181

Query Match 68.0%; Score 17; DB 10; Length 8;  
Best Local Similarity 28.6%; Pred. No. 1.2e+06;  
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVXH 7  
:::|:|  
DB 1 HRRKVLH 7

RESULT 25  
US-10-387-957-7  
; Sequence 7, Application US/10387957  
; Publication No. US20040052809A1  
; GENERAL INFORMATION:  
; APPLICANT: GlaxoSmithKline Biologicals s.a.  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45284  
; CURRENT APPLICATION NUMBER: US/10/387,957  
; CURRENT FILING DATE: 2003-03-13  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-387-957-7

Query Match 68.0%; Score 17; DB 12; Length 8;  
Best Local Similarity 33.3%; Pred. No. 1.2e+06;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 QXXVXH 7  
:::|:|  
DB 1 QGYMKH 6

RESULT 26  
US-10-014-340-64  
; Sequence 64, Application US/10014340  
; Publication No. US20030064411A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, et al  
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including  
; FILE REFERENCE: 9195-078  
; CURRENT APPLICATION NUMBER: US/10/014,340  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 823  
; SOFTWARE: Patentin Version 3.0  
; SEQ ID NO 64  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-014-340-64

Query Match 68.0%; Score 17; DB 12; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.2e+06;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 XYXHI 8  
:::|:|

DB 1 AVLHV 5

RESULT 27  
US-10-182-252A-624  
; Sequence 624, Application US/10182252A  
; Publication No. US20040072162A1  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; APPLICANT: BRUNAK, SOREN  
; APPLICANT: BUS, SOREN  
; APPLICANT: CORBET, SYLVIE  
; APPLICANT: LAUEKOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; FILE REFERENCE: 030307/0205  
; CURRENT APPLICATION NUMBER: US/10/182,252A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: EP 00610017.6  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/179,333  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 624  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-624

Query Match 68.0%; Score 17; DB 12; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.2e+06;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 XYXHI 8  
:::|:|  
DB 1 IICHI 5

RESULT 28  
US-10-182-252A-625  
; Sequence 625, Application US/10182252A  
; Publication No. US20040072162A1  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; APPLICANT: BRUNAK, SOREN  
; APPLICANT: BUS, SOREN  
; APPLICANT: CORBET, SYLVIE  
; APPLICANT: LAUEKOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; FILE REFERENCE: 030307/0205  
; CURRENT APPLICATION NUMBER: US/10/182,252A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: EP 00610017.6  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/179,333  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 625  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-625

Query Match 68.0%; Score 17; DB 12; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.2e+06;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 XVXHI 8  
: : : : :  
DB 1 IIGHI 5

RESULT 29  
US-10-328-953-94

Sequence 94, Application US/10328953  
Publication No. US20040071656A1  
GENERAL INFORMATION:  
APPLICANT: Wieland, Felix  
APPLICANT: Hartl, Franz-Ulrich  
TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies  
FILE REFERENCE: 11390/46101  
CURRENT APPLICATION NUMBER: US/10/328,953  
PRIOR FILING DATE: 2002-12-23  
PRIOR APPLICATION NUMBER: US 60/342,570  
PRIOR FILING DATE: 2001-12-26  
PRIOR APPLICATION NUMBER: US 60/343,884  
PRIOR FILING DATE: 2001-12-28  
PRIOR APPLICATION NUMBER: US 60/372,620  
PRIOR FILING DATE: 2002-04-12  
PRIOR APPLICATION NUMBER: US 60/399,342  
PRIOR FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: US 60/414,834  
PRIOR FILING DATE: 2002-09-28  
NUMBER OF SEQ ID NOS: 331  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 94  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: peptide in m13 coliphage  
US-10-328-953-94

Query Match 68.0%; Score 17; DB 12; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.2e+06;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 XVXHI 8  
: : : : :  
DB 1 TVQHV 5

RESULT 30  
US-10-367-580-186

Sequence 186, Application US/10367580  
Publication No. US20040071720A1  
GENERAL INFORMATION:  
APPLICANT: Rothman, James E.  
APPLICANT: Hartl, F. Ulrich  
APPLICANT: Hoe, Mee H.  
APPLICANT: Houghton, Alan  
APPLICANT: Takechi, Yoshizumi  
APPLICANT: Mayhew, Mark  
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies  
FILE REFERENCE: 11746/461061  
CURRENT APPLICATION NUMBER: US/10/367,580  
CURRENT FILING DATE: 2003-02-14  
PRIOR APPLICATION NUMBER: US 09/794,832  
PRIOR FILING DATE: 2001-02-27  
PRIOR APPLICATION NUMBER: US 09/011,645  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: PCT/US96/13363  
PRIOR FILING DATE: 1996-08-16

PRIOR APPLICATION NUMBER: US 60/002,490  
PRIOR FILING DATE: 1995-08-18  
PRIOR APPLICATION NUMBER: US 60/002,479  
PRIOR FILING DATE: 1995-08-18  
NUMBER OF SEQ ID NOS: 349  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 186  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-10-367-580-186

Query Match 68.0%; Score 17; DB 12; Length 8;  
Best Local Similarity 28.6%; Pred. No. 1.2e+06;  
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XQXXVX 7  
: : : : :  
DB 1 WRTGVFH 7

RESULT 31  
US-10-367-580-234

Sequence 234, Application US/10367580  
Publication No. US20040071720A1  
GENERAL INFORMATION:  
APPLICANT: Rothman, James E.  
APPLICANT: Hartl, F. Ulrich  
APPLICANT: Hoe, Mee H.  
APPLICANT: Houghton, Alan  
APPLICANT: Takechi, Yoshizumi  
APPLICANT: Mayhew, Mark  
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies  
FILE REFERENCE: 11746/461061  
CURRENT APPLICATION NUMBER: US/10/367,580  
CURRENT FILING DATE: 2003-02-14  
PRIOR APPLICATION NUMBER: US 09/794,832  
PRIOR FILING DATE: 2001-02-27  
PRIOR APPLICATION NUMBER: US 09/011,645  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: PCT/US96/13363  
PRIOR FILING DATE: 1996-08-16  
PRIOR APPLICATION NUMBER: US 60/002,490  
PRIOR FILING DATE: 1995-08-18  
PRIOR APPLICATION NUMBER: US 60/002,479  
PRIOR FILING DATE: 1995-08-18  
NUMBER OF SEQ ID NOS: 349  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 234  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-10-367-580-234

Query Match 68.0%; Score 17; DB 12; Length 8;  
Best Local Similarity 16.7%; Pred. No. 1.2e+06;  
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XVXHI 8  
: : : : :  
DB 3 QGIRHV 8

RESULT 32  
US-10-367-593-186

Sequence 186, Application US/10367593  
Publication No. US20040071721A1  
GENERAL INFORMATION:  
APPLICANT: Rothman, James E.

```

/ APPLICANT: Hartl, F. Ulrich
/ APPLICANT: Hoe, Mee H.
/ APPLICANT: Houghton, Alan
/ APPLICANT: Takechi, Yoshizumi
/ APPLICANT: Mayhew, Mark
/ TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
/ FILE REFERENCE: 11746/461012
/ CURRENT APPLICATION NUMBER: US/10/367,593
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: US 09/011,645
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: PCT/US96/13363
/ PRIOR FILING DATE: 1996-08-16
/ PRIOR APPLICATION NUMBER: US 60/002,490
/ PRIOR FILING DATE: 1995-08-18
/ PRIOR APPLICATION NUMBER: US 60/002,479
/ PRIOR FILING DATE: 1995-08-18
/ NUMBER OF SEQ ID NOS: 349
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 186
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-367-593-186

```

```

Query Match      68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 XQXXVXH 7
       ::::|:|
Db      1 WRTGVFH 7

```

```

RESULT 33
US-10-367-593-234
/ Sequence 234, Application US/10367593
/ Publication No. US20040071721A1
/ GENERAL INFORMATION:
/ APPLICANT: Rothman, James E.
/ APPLICANT: Hartl, F. Ulrich
/ APPLICANT: Hoe, Mee H.
/ APPLICANT: Houghton, Alan
/ APPLICANT: Takechi, Yoshizumi
/ APPLICANT: Mayhew, Mark
/ TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
/ FILE REFERENCE: 11746/461012
/ CURRENT APPLICATION NUMBER: US/10/367,593
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: US 09/011,645
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: PCT/US96/13363
/ PRIOR FILING DATE: 1996-08-16
/ PRIOR APPLICATION NUMBER: US 60/002,490
/ PRIOR FILING DATE: 1995-08-18
/ PRIOR APPLICATION NUMBER: US 60/002,479
/ PRIOR FILING DATE: 1995-08-18
/ NUMBER OF SEQ ID NOS: 349
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 234
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-367-593-234

```

```

Query Match      68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 16.7%; Pred. No. 1.2e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 XXVXHI 8
       ::::|:|
Db      3 QGIXHV 8

```

```

RESULT 34
US-10-367-594-186
/ Sequence 186, Application US/10367594
/ Publication No. US20040071722A1
/ GENERAL INFORMATION:
/ APPLICANT: Rothman, James E.
/ APPLICANT: Hartl, F. Ulrich
/ APPLICANT: Hoe, Mee H.
/ APPLICANT: Houghton, Alan
/ APPLICANT: Takechi, Yoshizumi
/ APPLICANT: Mayhew, Mark
/ TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
/ FILE REFERENCE: 11746/461041
/ CURRENT APPLICATION NUMBER: US/10/367,594
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: US 09/580,806
/ PRIOR FILING DATE: 2000-10-05
/ PRIOR APPLICATION NUMBER: US 09/011,645
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: PCT/US96/13363
/ PRIOR FILING DATE: 1996-08-16
/ PRIOR APPLICATION NUMBER: US 60/002,490
/ PRIOR FILING DATE: 1995-08-18
/ PRIOR APPLICATION NUMBER: US 60/002,479
/ PRIOR FILING DATE: 1995-08-18
/ NUMBER OF SEQ ID NOS: 349
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 186
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-367-594-186

```

```

Query Match      68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 XQXXVXH 7
       ::::|:|
Db      1 WRTGVFH 7

```

```

RESULT 35
US-10-367-594-234
/ Sequence 234, Application US/10367594
/ Publication No. US20040071722A1
/ GENERAL INFORMATION:
/ APPLICANT: Rothman, James E.
/ APPLICANT: Hartl, F. Ulrich
/ APPLICANT: Hoe, Mee H.
/ APPLICANT: Houghton, Alan
/ APPLICANT: Takechi, Yoshizumi
/ APPLICANT: Mayhew, Mark
/ TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
/ FILE REFERENCE: 11746/461041
/ CURRENT APPLICATION NUMBER: US/10/367,594
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: US 09/580,806
/ PRIOR FILING DATE: 2000-10-05
/ PRIOR APPLICATION NUMBER: US 09/011,645
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: PCT/US96/13363
/ PRIOR FILING DATE: 1996-08-16
/ PRIOR APPLICATION NUMBER: US 60/002,490
/ PRIOR FILING DATE: 1995-08-18
/ PRIOR APPLICATION NUMBER: US 60/002,479

```

PRIOR FILING DATE: 1995-08-18  
NUMBER OF SEQ ID NOS: 349  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 234  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-10-367-594-234

Query Match 68.0%; Score 17; DB 12; Length 8;  
Best Local Similarity 16.7%; Pred. No. 1.2e+06;  
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 8  
DB 3 QGIXHV 8

## RESULT 36

US-10-367-654-186  
Sequence 186, Application US/10367654  
Publication No. US20040071723A1  
GENERAL INFORMATION:  
APPLICANT: Rothman, James E.  
APPLICANT: Hartl, F. Ulrich  
APPLICANT: Hoe, Mee H.  
APPLICANT: Houghton, Alan  
APPLICANT: Takeuchi, Yoshizumi  
APPLICANT: Mayhew, Mark  
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies  
FILE REFERENCE: 11746/461032  
CURRENT APPLICATION NUMBER: US/10/367,654  
CURRENT FILING DATE: 2003-02-14  
PRIOR APPLICATION NUMBER: US 10/171,734  
PRIOR FILING DATE: 2002-06-13  
PRIOR APPLICATION NUMBER: US 09/636,295  
PRIOR FILING DATE: 2000-08-10  
PRIOR APPLICATION NUMBER: US 09/011,645  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: PCT/US96/13363  
PRIOR FILING DATE: 1996-08-16  
PRIOR APPLICATION NUMBER: US 60/002,490  
PRIOR FILING DATE: 1995-08-18  
PRIOR APPLICATION NUMBER: US 60/002,479  
PRIOR FILING DATE: 1995-08-18  
NUMBER OF SEQ ID NOS: 349  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 186  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-10-367-654-186

Query Match 68.0%; Score 17; DB 12; Length 8;  
Best Local Similarity 28.6%; Pred. No. 1.2e+06;  
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 XOXVXH 7  
DB 1 WRTGVFH 7

## RESULT 37

US-10-367-654-234  
Sequence 234, Application US/10367654  
Publication No. US20040071723A1  
GENERAL INFORMATION:  
APPLICANT: Rothman, James E.  
APPLICANT: Hartl, F. Ulrich

APPLICANT: Hoe, Mee H.  
APPLICANT: Houghton, Alan  
APPLICANT: Takeuchi, Yoshizumi  
APPLICANT: Mayhew, Mark  
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies  
FILE REFERENCE: 11746/461032  
CURRENT APPLICATION NUMBER: US/10/367,654  
CURRENT FILING DATE: 2003-02-14  
PRIOR APPLICATION NUMBER: US 10/171,734  
PRIOR FILING DATE: 2002-06-13  
PRIOR APPLICATION NUMBER: US 09/636,295  
PRIOR FILING DATE: 2000-08-10  
PRIOR APPLICATION NUMBER: US 09/011,645  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: PCT/US96/13363  
PRIOR FILING DATE: 1996-08-16  
PRIOR APPLICATION NUMBER: US 60/002,490  
PRIOR FILING DATE: 1995-08-18  
PRIOR APPLICATION NUMBER: US 60/002,479  
PRIOR FILING DATE: 1995-08-18  
NUMBER OF SEQ ID NOS: 349  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 234  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-10-367-654-234

Query Match 68.0%; Score 17; DB 12; Length 8;  
Best Local Similarity 16.7%; Pred. No. 1.2e+06;  
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 XXVXH 8  
DB 3 QGIXHV 8

## RESULT 38

US-10-367-658-186  
Sequence 186, Application US/10367658  
Publication No. US20040071724A1  
GENERAL INFORMATION:  
APPLICANT: Rothman, James E.  
APPLICANT: Hartl, F. Ulrich  
APPLICANT: Hoe, Mee H.  
APPLICANT: Houghton, Alan  
APPLICANT: Takeuchi, Yoshizumi  
APPLICANT: Mayhew, Mark  
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies  
FILE REFERENCE: 11746/461031  
CURRENT APPLICATION NUMBER: US/10/367,658  
CURRENT FILING DATE: 2003-02-14  
PRIOR APPLICATION NUMBER: US 09/794,529  
PRIOR FILING DATE: 2001-02-27  
PRIOR APPLICATION NUMBER: US 09/011,645  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: PCT/US96/13363  
PRIOR FILING DATE: 1996-08-16  
PRIOR APPLICATION NUMBER: US 60/002,490  
PRIOR FILING DATE: 1995-08-18  
PRIOR APPLICATION NUMBER: US 60/002,479  
PRIOR FILING DATE: 1995-08-18  
NUMBER OF SEQ ID NOS: 349  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 186  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-10-367-658-186

```
Query Match      68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 XXVXVXH 7
      :|:|:|:|
Db      1 WRTGVFH 7

RESULT 39
US-10-367-658-234
; Sequence 234, Application US/10367658
; Publication No. US20040071724A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461051
; CURRENT APPLICATION NUMBER: US/10/367,658
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,529
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 234
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-658-234

Query Match      68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 16.7%; Pred. No. 1.2e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      3 XXVXVXH 8
      :|:|:|:|
Db      3 OGIXHV 8

RESULT 40
US-10-367-668-186
; Sequence 186, Application US/10367668
; Publication No. US20040071725A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461072
; CURRENT APPLICATION NUMBER: US/10/367,668
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,517
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
```

```
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 186
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-668-186

Query Match      68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 XXVXVXH 7
      :|:|:|:|
Db      1 WRTGVFH 7

RESULT 41
US-10-367-668-234
; Sequence 234, Application US/10367668
; Publication No. US20040071725A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461072
; CURRENT APPLICATION NUMBER: US/10/367,668
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,517
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 234
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-668-234

Query Match      68.0%; Score 17; DB 12; Length 8;
Best Local Similarity 16.7%; Pred. No. 1.2e+06;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      3 XXVXVXH 8
      :|:|:|:|
Db      3 OGIXHV 8

RESULT 42
US-10-139-146-66
; Sequence 66, Application US/10139146
; Publication No. US20030099932A1
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/ GENERAL INFORMATION:
/ APPLICANT: LORENS, James B.
/ TITLE OF INVENTION: RETROVIRAL VECTORS WITH SEPARATION SEQUENCES
/ FILE REFERENCE: A-70980/RMS/CYO
/ CURRENT APPLICATION NUMBER: US/10/139,146
/ CURRENT FILING DATE: 2003-01-22
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 66
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Rasmhead rat sarcoma virus
US-10-139-146-66

Query Match      68.0%; Score 17; DB 14; Length 8;
Best Local Similarity 28.6%; Pred. No. 1.2e+06;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 XXXXXH 7
       11111
DB      2 GGLTTH 8

RESULT 43
US-10-052-578-13
/ Sequence 13, Application US/10052578
/ Publication No. US20030134787A1
/ GENERAL INFORMATION:
/ APPLICANT: Sloan-Kettering Institute for Cancer Research
/ APPLICANT: Rothman, James E.
/ APPLICANT: Mayhew, Mark
/ APPLICANT: Hoe, Mee H.
/ APPLICANT: Houghton, Alan
/ APPLICANT: Hartl, Ulrich
/ APPLICANT: Ouerfell, Quatchek
/ APPLICANT: Moroi, Yoichi
/ TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
/ FILE REFERENCE: 11746/46003
/ CURRENT APPLICATION NUMBER: US/10/052,578
/ CURRENT FILING DATE: 2002-01-17
/ PRIOR APPLICATION NUMBER: 08/961,707
/ PRIOR FILING DATE: 1997-10-31
/ NUMBER OF SEQ ID NOS: 321
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 13
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: peptide in m13 coliphage
US-10-052-578-13

Query Match      68.0%; Score 17; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 YXXHI 8
       11111
DB      1 TVQHV 5

RESULT 44
US-10-053-520-13
/ Sequence 13, Application US/10053520
/ Publication No. US20030166530A1
/ GENERAL INFORMATION:
/ APPLICANT: Sloan-Kettering Institute for Cancer Research
/ APPLICANT: Rothman, James E.
/ APPLICANT: Mayhew, Mark
/ APPLICANT: Hoe, Mee H.
/ APPLICANT: Houghton, Alan
/ APPLICANT: Hartl, Ulrich
/ APPLICANT: Ouerfell, Quatchek
```

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/ APPLICANT: Moroi, Yoichi
/ TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
/ FILE REFERENCE: 11746/46004
/ CURRENT APPLICATION NUMBER: US/10/053,520
/ CURRENT FILING DATE: 2002-10-01
/ PRIOR APPLICATION NUMBER: 08/961,707
/ PRIOR FILING DATE: 1997-10-31
/ NUMBER OF SEQ ID NOS: 321
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 13
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: peptide in m13 coliphage
US-10-053-520-13

Query Match      68.0%; Score 17; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 YXXHI 8
       11111
DB      1 TVQHV 5

RESULT 45
US-10-053-498B-13
/ Sequence 13, Application US/10053498B
/ Publication No. US20030194409A1
/ GENERAL INFORMATION:
/ APPLICANT: Sloan-Kettering Institute for Cancer Research
/ APPLICANT: Rothman, James E.
/ APPLICANT: Mayhew, Mark
/ APPLICANT: Hoe, Mee H.
/ APPLICANT: Houghton, Alan
/ APPLICANT: Hartl, Ulrich
/ APPLICANT: Ouerfell, Quatchek
/ APPLICANT: Moroi, Yoichi
/ TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
/ FILE REFERENCE: 11746/46002
/ CURRENT APPLICATION NUMBER: US/10/053,498B
/ CURRENT FILING DATE: 2002-01-17
/ PRIOR APPLICATION NUMBER: 08/961,707
/ PRIOR FILING DATE: 1997-10-31
/ NUMBER OF SEQ ID NOS: 321
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 13
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: peptide in m13 coliphage
US-10-053-498B-13

Query Match      68.0%; Score 17; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 YXXHI 8
       11111
DB      1 TVQHV 5

Search completed: August 19, 2004, 16:00:18
Job time : 38 secs
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